

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 19, 2002, 07:56:52 ; Search time 48 Seconds  
 (without alignments)  
 2343.753 Million cell updates/sec

Title: US-09-807-459-2  
 Perfect score: 2359  
 Sequence: 1 MAPSDVGDVTKTLLAASES.....DP SKALIRKVSTEADNILEK 458

Scoring table: BLOSUM62

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Ygapop	10.0	' Ygapext	0.5
Fgapop	6.0	' Fgapext	7.0
Delop	6.0	' Delext	7.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767056

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=issued_Patents_NA -QMT=fastap -SUFFIX=rnl -MNMATCH=0.1 -IDOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGNE=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=10
-MODE=LOCAL -OUTFMT=PTO -NORM=0 -HEAPSIZE=500 -MINTLEN=0 -MAXLEN=2000000000
-USER=US09807459 @CGN_1_113_6runat_18102002_141113_28610 -NCPU=6 -ICPU=3
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-WARN TIMEOUT=10 -THREADS=1 -XGAPEXT=0.5 -XGAPOP=6 -XGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Database : Issued Patents\_NA:  
 1: /cgn2.6/ptodata/2/ina/5A\_COMBO.seq: \*  
 2: /cgn2.6/ptodata/2/ina/5B\_COMBO.seq: \*  
 3: /cgn2.6/ptodata/2/ina/6A\_COMBO.seq: \*  
 4: /cgn2.6/ptodata/2/ina/6B\_COMBO.seq: \*  
 5: /cgn2.6/ptodata/2/ina/PC10US\_COMBO.seq: \*  
 6: /cgn2.6/ptodata/2/ina/backfiles1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
1	827.5	35.1	1962	1 US-07-803-636A-1
2	826.5	35.0	1990	6 5171685-5
3	826.5	35.0	1990	6 551916
4	5.1	3883	1 US-08-468-036-33	
5	120	5.1	3883	2 US-08-376-843-33
6	120	5.1	3884	4 US-09-541-822-3
7	119.5	5.1	4766	5 PCT-US93-07261-10
8	111	4.7	3278	1 US-08-484-015-13
9	111	4.7	3278	1 US-08-484-016-13
10	108.5	4.6	756	2 US-09-569-869-2
11	108.5	4.6	7568	3 US-09-349-846-2
12	105.5	4.5	1766	2 US-08-453-848-8

**ALIGNMENTS**

RESULT 1  
 US-07-803-636A-1  
 ; Sequence 1, Application US/07803636A  
 ; Patent No. 5422428  
 ; GENERAL INFORMATION:  
 ; APPLICANT: McGuire, Travis C., Terry F. McElwain, Lance E. Perriman,  
 ; ATTORNEY: William C. Davis  
 ; TITLE OF INVENTION: IMMUNIZATION AGAINST BABESIOSIS USING  
 ; TITLE OF INVENTION: PURIFIED SURFACE ANTIGENS OF BABESIA BIGEMINA AND SIMILAR  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: David R. SALIWANCHIK  
 ; STREET: 2421 NW 41ST STREET, SUITE A-1  
 ; CITY: GAINESVILLE  
 ; STATE: FLORIDA  
 ; COUNTRY: USA  
 ; ZIP: 32606  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version 1.1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/803, 636A  
 ; FILING DATE: 19911206  
 ; CLASSIFICATION: 424  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: SALIWANCHIK, DAVID R  
 ; REGISTRATION NUMBER: 31,794  
 ; REFERENCE/DOCKET NUMBER: WA4-059.C1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 904-375-8100  
 ; TELEFAX: 904-372-5800  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS: 1:

LENGTH: 1962 base pairs  
 TYPE: NUCLEAR ACID  
 STRANDEDNESS: both  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: BABESIA BIGEMINA  
 STRAIN: JG-29  
 INDIVIDUAL ISOLATE: MEXICO  
 CELL TYPE: MEROZOITE  
 IMMEDIATE SOURCE:  
 CLONE: PB958  
 FEATURE: CDS  
 NAME/KEY: CDS  
 LOCATION: 186..1628  
 FEATURE:  
 NAME/KEY: sig\_peptide  
 LOCATION: 186..248  
 FEATURE:  
 NAME/KEY: polyA\_site  
 LOCATION: 1884..1889

US-07-803-636A-1

Alignment Scores:  
 Pred. No.: 1.39e-92  
 Score: 827.50  
 Percent Similarity: 59.12%  
 Best. Local Similarity: 41.80%  
 Query Match: 35.08%

US-09-807-459-2 (1-458), x US-07-803-636A-1 (1-1962)

Qy 4 SerAspSerValGlyAspValThrLysIleuLeuAlaAlaSerGluSerValAspSer 23  
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 Db 282 GCAAGGGTGGTGGAGATGTCGAAAGACCTTGCTGGAAAGCCTAGGTTGAGCTGCAATGCT 341.  
 Qy 24 AlaAlaAsnAlaTyrMetLeasnSerAspMetSerAspTyrIleuSerAlaValSerAsp 43  
 ::||||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| 401.  
 Db 342 GAAATGGAGCAACATCAGGTCAACAAAGATATGCAAACTCATGTCATGTTAAGG 401.  
 Qy 44 AsnAspHeAlaGluArgIleCysSerGlnValProLysGlySerAsnCysSerAlaSerVal 63  
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| 461.  
 Db 402 ACCCTTGTTGGTGGAGGCTGCGGAGAAAGTTGCTGGAAACTCTACCTGGGTGAGAGCGTA 63.  
 Qy 64 SerAlaTyrMetSerAspCysAlaAlaLysGlnAspCysLeuThrIleuGinSerAlaLysIleu 83  
 ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| 515.  
 Db 462 ATTGCCCTAAGTTAACGCTGGTGAAGGAGGGCATGACGCCTGACAGCANG----- 515.  
 Qy 84 ProLeuGluIaLysTyrGlnProLeuThrLeuProAspProTyrglnLeuGluAlaAla 103  
 ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| 563.  
 Db 516 -----AGTACAAGGCCGGTGAACCTTACCCCTCGGAAGAATGGGCTTCCTGG 623.  
 Qy 104 PheLeuLeuPhelysGluSerAspAlaAsnProAlaAsnSerThrLysGluAspPheAsp 123.  
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 Qy 124 MetArgPheArgArgGlyLysAsnHisSerTyrPheHsAspIleuValPheAsnLeuLeu 143.  
 ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| 677.  
 Db 624 ATGGCTTCGAGG-----AGCAGCCACGCCGACACTTGCATGAGACTTGACATGCCAGTAC 677.  
 Qy 144 GluIysAsnValThrArgAspAlaAspAlaIleuAspIleuGluAsnPheAlaSerArgTyr 163.  
 ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| 737.  
 Db 678 AAGAGAGAATGCTGACGGACCCCTGGAATCCATGATGTTGAGACTTGACATGCCAGTAC 737.  
 Qy 164 LeuIyrmEtaLalThrLeuIyrmIlyLysThrIyrmIlyLysThrAsnValAspGluPheGlyAlaSer 183.  
 ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| 797.  
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 Qy 184 PhePheAsnLysIleuSerPheThrIleuGlyIleuGlyTrpIleuLysAlaGalaeu 203.  
 ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| 6.

RESULT 2  
 5171685-5  
 ; Patent No. 5171685  
 ; APPLICANT: MCGUINN, TERRY F.; HINES, STEPHEN A.; MCGUIRE, TRAVIS C.; PALMER, GUY H.; JASNER, DOUGLAS P.; REDUKER, DAVID W.; GOFF, WILL L.; PERLMAN, LANCE E.; DAVIS, WILLIAM C.  
 ; TITLE OF INVENTION: CLONING OF THE BABESIA BOVIS 60 KD ANTIGEN  
 ; NUMBER OF SEQUENCES: 7  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/504,461  
 ; FILING DATE: 04-APR-1990  
 ; SEQ ID NO: 5171685-5  
 ; LENGTH: 1990

Alignment Scores:  
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 Percent Similarity: 51.30%  
 Best Local Similarity: 35.53%  
 Query Match: 35.04%  
 DB: 6 Gaps: 6

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 Db 858 AAGGTTTGTGTTAGGAGCACCTTCCTGTTGACCTGGAAAC---CACCTGAGGCCACC 914.  
 Qy 224 LeuGlnHisIleThrSerSerTyrLysAspTyrMetAspIleuGlnIleProAlaLeuPro 243.  
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 Db 915 ATCCGCGAAATAGCTAGCGCTACGGCAGTAGATGATGAGCTGGATGAC 974.  
 Qy 244 LysheAlaLysArgPhosSerLeuMetValValGlnArgLeuAlaThrValAlaLys 263.  
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 Db 975 TCGTmCGCmGAGCTTTCmCmCAAGTGGCTACTAAAGCTCTGTTGTTACCGTCAGGCAC 1034.  
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 Db 1035 TACCTCCATTGCGCGCTGAGAGGGTGTAGAGGAAGTCAGGATTCAAGGATTCACTGTCAC 1094.  
 Qy 284 ArgGlyAlaIleProThrLysAspPheAsnLysGluIleArgGluProSerLys--- 302.  
 ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| 1211.  
 Db 1095 --TTCTTACTGACCCCTCCAACTGTGATTATGAGCAGCACGCTCTCAGCCCTGTAAGCT 1151.  
 Qy 303 AlaLeuLysGluLysValSerThrAspThrLysAspIleuPheGluAsnLysIleGlyGln 322.  
 ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| 322.  
 Db 1152 GGCCTACACAAAGCmGmGCTCCCGAGAGCAGCAGGCTATCAGGAATGTCGGTCAA 1211.  
 Qy 323 GLyThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLys 342.  
 ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| 357.  
 Db 1212 AGCACCAAGCTATGCCAC---GGTGTAGPAGTTGTCAGGATGATGTAAGGAG--- 1265.  
 Qy 343 ValSerAsnAspAlaLysAlaPheGluAsnLysIleGly 356.  
 ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| 1266.  
 Db 1266 -----CCTACGACAAACAATAATTGCTGAGAGCTCCCTACTRACTCTTCAAGCA 1316.  
 Qy 357 GluGlyThrValAspPheIleAlaAsnAspGluIleArgAsp---ProSerLysAlaLeu 374.  
 ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| 1317.  
 Db 1317 AAUGGAGCGCTGTGAGCACGCTGTTAGAGGTTAAATCCGGTGTGCGCATAG 1370.  
 Qy 375 IleArgLysValSerThrIleGlyAlaIleGluAspPheGluAsnLysIleGlyGlyGlyThr 394.  
 ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| 1371.  
 Db 1371 --CAAAAGGGACCAACCTCCGAAGCAGCTGAGGAAACCGTTCCGTGCTGCG--- 1424.  
 Qy 395 ValAspHeAlaIleAsnAspGluIleArgAspProSerLysAlaLeuIleArgIleValTyr 414.  
 ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| 1425.  
 Db --GATTCGGGAAACTGATTGAGGTCCCTGAGAACAACTACGTCGATGCTGTTACT 1481.  
 Qy 415 Thr-----GluIaAspAspPasp 419.  
 ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| ::||||| 1482.  
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Qy	81	LeuLysTyrProleuGluAlaLysTrpGlnProleuThrIleProAspProTyrcleu
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Qy	101	GlutAlaAlaPhenIleLeuPhenLysGluSerAspAlaAsnProAlaAsnSerThrGluLys
Db	512	GATGCCGCTTCAGATGTCAGAGGAGGTCATGCCAACCTTACAGTG
Qy	121	ArgPheTrpMetArgPheAspGargGlyLysAsnHisSerTyrPheHisAspLeuValPhe
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Qy	141	AsnLeuLeuGluLysAlaValThrArgAspAlaAspAlaAspAlaThrAspIleGluAspHeAla
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Qy	161	SerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspGluPhe
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Qy	181	GlyAlaSerPhePheAsnLysLeuSerPheThrTyrGlyLeuPheGlyIlePheGlyLys
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Qy	201	ArgAlaLeuLysGlnIleLeuArgSerAspLeuProLeuAspIleGlyLysThrGluLys
Db	812	CAAACATGGTGTGATTCATCAGGGGAATGTCCTGAGATTGTTGAGATTG
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Qy	241	AlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThr
Db	929	ACTCTTTCAGTTGCACCGCTGTTATGCTGACATGGTGAAGAAGGTTCTGCTGGTASC
Qy	989	TGACCTCGTCTGCTGAACTCTCTGGTACAAAGATGGTAAAGAAATCAGACTT
Qy	261	ValAlaGlyLysValAspTrpProTrpTrpLysTrpTyrMetLysIleAspPhe
Db	988	TTGACCTCGTCTGCTGAACTCTCTGGTACAAAGATGGTAAAGAAATCAGACTT
Qy	281	MetValAsnArgValPheIleProThrLysPhe-----
Db	1049	TTCTCTAAAGTACCCACCTACAGAAAGTCTACAGGAGTACTAACGAGTTAC
Qy	292	-----
Db	1109	AAAACACTATCTGAAAGCCAAATGTTGCTGACGCCACTAAAGATTATGCCAGGACTCAC
Qy	293	-----PhenAsnLysGluIleArgGluProSerLysAlaLeuLysGlu-----
Db	1169	GGAAACACCAAGGCTATCTGAAAGAGAATCTAGCGAACCTACTAACAGTTTCAG
Qy	307	LysValSerThrAspThrLysAspLeuPheGluAsnLysIleGlyLysGlyLysValAsp
Db	1229	GAGGCCTCTAAGTCACCAACACACTCTTGATGAGAACATGGCCAACCCACCAAGAG
Qy	327	PhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLysValSerAsnAsp
Db	1289	TTCCTCAGGGAAAGCTCCCAAGCCACTAACATTCAGCTAACAGAACATGCCAACCA
Qy	347	AlaLysAspLeuPheGluAsnLysIleGlyLysGlyLysValAspPheIleAsnAsnGlu
Db	1349	ACCAGGAGTCTTC--AGGGAGGCTCTCAAGCCACTAACAGACTTCTCAGGGAGAA
Qy	367	IleArgAspProSerLysAlaLeuIleArgLysValSerThrGlyAlaGluAspLeuPhe
Db	111	-----

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Db          1406 ATTTGCTCAACCTACTAAAGAATTTCAGGATGTCCTCAAGTCACCA
Qy          387 GluAsnLysIleGlyGlnGlyThrValAspPhe-
Db          1466 ACTGAGAACATGCTCAACCAACTAAGGATGTCGGAGGGTTCTC
Qy          398 -----IleAsnGluIleArgAspProSerLysAlaLeuIleArg
Db          1526 AAAGTCITGATGAAACATGTCACACTGCCAGGAATCATACAT
Qy          416 GluAlaAspAspLeuPheGluAsnLysIleGlyGlnGlyThrValAsp
Db          1586 GCGGCCAAAGAT--TCATTCGGCAGCCCCATGAGGACTAAGCAG
Qy          436 GluIleArgAspProSerLysAlaLeuIleArg--LysValSerThr
Db          1643 ACTGTTGCCAACCTACAGAGGATTCTGAAACGGAGCTTGAAGACT
Qy          455 Leu 455
Db          1703 TTA 1705
Db          1703 TTA 1705

RESULT 4
US-08-468-036-33
; Sequence 33, Application US/08468036
; Patent No. 5,728806
; GENERAL INFORMATION:
; APPLICANT: Demaggio, Anthony J.
; APPLICANT: Hoeksma, Merit F.
; TITLE OF INVENTION: Materials and Methods Relating to
; TITLE OF INVENTION: Interact with Casein Kinase I
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Beck
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468, 036
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/184, 605
; FILING DATE: 21-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5728806 and Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31784
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3883 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-468-036-33

Alignment Scores:
Pred. No.: 0.000286 Length: 3883
Score: 120.00 Matches: 121
Percent Similarity: 34.7% Conservative: 92
Best Local Similarity: 19.748 Mismatches: 214

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/376, 843

FILING DATE: 21-JAN-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/184, 605

REFERENCE/DOCKET NUMBER: 35, 302

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6300

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 3883 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

Alignment Scores:

Ref. No.:	0.000286	Length:	3883
Score:	120.00	Matches:	121
Conservat.:	34.75%	Conservative:	92
Local Similarity:	19.74%	Mismatches:	214
Query Match:	5.09%	Delets:	186
		Gaps:	29

(1-458) x US-08-376-843-33 (1-3883)

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b 1051 AGGGATGGAGCGGAATTATACCCAGGGTCTTGAAGTTGACACATTGGAACTA 110

b 24 AlaAlaAspAlaAspMetLeu-----AsnSerAspMetSer 35

b 1111 CAAAGAGAACGATTCGAGTAAATGTTGCTCATGAACTCTAACGAGAAATGAAAG 1170

b 36 AspPyrLeuSerAlaValSerAsp-----AsnHeAla 46

b 1171 GGTCTCTTGACAGCAATGACACGGCTCTAGTAACTGGTTGACGGCAATTATG 1230

b 47 GluArgLeuCysSerGlnValProLysGlySerAsnCysSerAlaSerValSerAla 66

b 1231 AAAAATGTTGAGATTTCGCTCAAGCACAGAAATAAACACTAGCACAGTCGCTAGT 1290

b 67 MetSerAspGlyAspAlaLysInaAspCys-----LeuThrLeuGln 79

b 1291 AGTTCAGGAGTAATCTAGGAAGCTCTCCGAGTCATTAAATGATCTAACCTAA 1350

b 80 Ser-----LeuLysTyrProLeuGluAlaLysTyrGlnProLeuThrLeuProAspPro 97

b 1351 GCTCTCTATGAAAGGTTAGGACAAATCACTGGCAATTACCAAGCACAG 1410

b 98 TyrGlnLeuGluAlaAlaPhenLeuPhenLysGluSerAspAlaAsnProAlaAsn 117

b 1411 TATCAACACACAGGCACTGGAATCCGAGAACACTCTCTCAACTCTGGCTTAC 1470

b 118 Thrglu-----LysAspGlyAspPheAspMetArgPhe 126

b 1471 ACTATAATGCTCTAGTACCAACACAATAACGGTCAGAAGTTCGATGGCTCA 1530

b 127 ArgArgGlyLysAsnHisSerTyrPheHisAspLeuVal----- 139

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Qy 140 -----PheAsnLeuLeuGluLysAsnValThr---ArgAspAlaAspAlaThrAsp 155

Db 1591 ATGGAGGGCTAACCTATTACAAAGCTTAAGCATAGGCAGTAGCGTCACCTAA 1650

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Qy 177 ValAspGluPheGly-----AlaSerPhePheAsnLysLeu 188

Db 1771 ATCAACACATCCGAGCATTAATCACGTGCCAAGGAAGCTGGCTCAACCAAAGT 1830

Qy 174 Tyr-----ThrAsn 176

Db 1711 CAGCATGAACTATTAGAATTGAACTTCGACATCTGTTGATTTAGCTGTTCAAGAAC 1770

Qy 189 SerPheThrThrGly-----Val 193

Db 1831 CTATTGACGCCGGCCTAAACGCACTCGTAGATAAAGGCCATATACCTTC 1890

Qy 194 -----LeuPheGlyTyrPheLysLeuArgAla 202

Db 1891 CGTGAATGCAATGACCCGCCTCTCTCAAGATRCCCTGGTGTAAATGAAACCGCA 1950

Qy 203 LeuLysGlnIleLeuArgSerAsnLeuProLeuAspIleGlyThrGluHisSerValSer 222

Db 1951 CTA-----ArgGluCTACTATATGCTGCTGCCAAAGTAACCTGAGAACCTGAGT 2001

Qy 223 ArgLeuGlnHistLeuThrSerSerTyrLysAspTyrMetAspThrGlnIleProAlaLeu 242

Qy 244 ArgLysGlnIleLeuAspSerAsnLeuProLeuAspIleGlyThrGluHisSerValSer 222

Db 2002 ACATTAAGCT-----GCCTCGAAGCTAAACATTAGAACAG-----CCGCACTG 2052

Qy 243 ProLysPheAlaLysArgPheSerLeuMet-----Val 253

Db 2053 GGTCTCTATAATGAGGATATTGGTTAAATAACTATGGAAATTAGCAAGATT 2112

Qy 254 ValGlnArgLeuLeuAlaThrValAlaGly-----TyrValAspThrProPheTyr 270

Db 2113 AAATGCCATTACTCTCTACAAAGAAGGATAATATGACGCCAGATCCTAC 2172

Qy 271 LysLysTyrPheMetLysLeuLysAsnPheMetValAspArgValGlyLeuProThrLys 290

Db 2173 AAAAATGAACTGAGTTGAGTTAA-----AATGAACT----- 2214

Qy 291 LysPhePheAsnLysGlyIleLeuArgGluProSerLysAlaLeuLysGlyLysValSerThr 310

Db 2215 -----GAGAACTGTTAAGAGGAATGAGTTGACATGCAAATGCAATG 2262

Qy 311 AspThrLysAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheAsnLys 330

Db 2263 CTAGTAAAGATAATTGAGTCAAA-----GAAACTATTCATCTCAAATTCG 2313

Qy 331 GluLeuGlyAspProSerLysAlaLeu-----LysGlu 341

Db 2314 CAATAGAATCATGAAACTACCATGATCATTAAGGCAACACTAGATAACAGCAT 2373

Qy 342 LysValSerAsnSpaPheLysAspLeuPheGluLysIleGlyGlnGlyThr----- 359

Db 2374 AAACCTGAATGAAATTCGGAT-----TTTAAATACAACTACAGAGTGTACTGGATA 2430

Qy 363 -----IleAsnAsnGluLeuAspProSerLysAlaLeuIleArgLysValSerThr 380

Qy 360 -----ValAspPhe----- 362

Db 2491 ATGCATAATGCCCTTACATGATTACAAAGAAGACTTGACCTTAATCAAAGTTGAA 2550

Db 2431 ATGCAAATGCCCTTACATGATTACAAAGAAGACTTGACCTTAATCAAAGTTGAA 2490

Qy 381 GlyAlaGluAsp-----LeuPheGluAsnLysIleGlyGlnGlyThrValAspPhe 398

Db 2551 ATGCCACAGGAAGATGTTCTCAAGAGCAATTCACCTGATGATGATC 2607

Qy 399 AsnasnGluileArgaspproSerlysAlaLeu----- 409  
Db 2608 AAAATGAGTACGACTCTTATGAGAACATGAGAAAAGCTGAACATACTCTGACAA 2657  
Qy 410 -----IleArglysValTyrThrIgluAlaAspaspLeupheglu-----Asnlys 424  
Db 2668 GACTGTGAGAGAAATTAAAGGAATCTCTAAATCTCAATGTTATTGAGAA 2727  
Qy 425 IleGlyGlyGlyLysValTyrThrIgluAlaAspaspLeupheglu----- 139  
Db 2728 ATCCACATATAAGCTTCACAAATTATATAAAATAGCCAGAAT----- 2781  
**RESULT 6**  
US-09-541-782-3  
; Sequence 3, Application US/09541782  
; Patent No. 6284480  
; GENERAL INFORMATION:  
; APPLICANT: Nislow, Corey  
; APPLICANT: Sakowicz, Roman  
; APPLICANT: Beraud, Christophe  
; TITLE OF INVENTION: Antifungal Assay  
; FILE REFERENCE: 1015  
; CURRENT APPLICATION NUMBER: US/09/541,782  
; CURRENT FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: FastSeq for Windows version 4.0  
; SEQ ID NO: 3  
; LENGTH: 3184  
; TYPE: DNA  
; ORGANISM: *Saccharomyces cerevisiae*  
; US-09-541-782-3

Alignment Scores:

Pre<sup>d</sup> No.: 0.000287 Length: 3884  
Score: 120.00 Matches: 121  
Percent Similarity: 34.75% Conservative: 92  
Best Local Similarity: 19.74% Mismatches: 214  
Query Match: 5.09% Indels: 186  
DB: 4 Gaps: 29

US-09-807-459-2 (1-458) x US-09-541-782-3 (1-3884)

Qy 4 SeraspSerValGlyAspValThrIlysthrLeuAlaAlaserGluSerValAspSer 23  
Db 1052 AGCGATGAGCAGGAAATTAAACCGAGGGCTCTTGTGAAGTGTGACACATTGAACTA 1111  
Qy 24 AlaAlaAspAlaThrMetIle-----AsnSerAspMetSer 35  
Db 1112 CAACAGAACGATTCAGTAAAGTGTCTCACTGAACTCTACAAACGAGAAATGAG 1171  
Qy 36 AspTyrLeuSerAlaValSerAsp-----AshpheAla 46  
Db 1172 GACCTCTTGACACAAATGCAACGGCTCTAGTATACTGGCTTGACGCCATTG 1231  
Qy 47 GluThrGlyLeuGlySerGlnValProLysGlySerAsnCysSerAlaSerAlaThr 66  
Db 1232 AAAAATTGAGGAGTTGCTCAGCACAGCAATAATACCACTAGCAACAGCTG 1291  
Qy 67 MetSerArgCysAlaLysGinAspCys-----AspThrLeuGln 79  
Db 1292 AGTCAGGAGTAATCTAGAAAGTTCCTCGAGGTCAATTAAAGATCAACCTCAA 1351  
Qy 80 Ser-----LeuLysTyrProLeuGluAlaLysTyrGlnProLysThrLeuProAspPro 97  
Db 1352 GCTGCTCTATAAGAAAAGGTTAGGACAAATCACTGCCGAAATACCAACGACAG 1411  
Qy 98 TyrGlnLeuGluAlaAlaPheLeuPheLysGluSerAspAlaAsnProAlaAsn 117

Db 1412 TATCACACAAACAGCAGTGAATTCCAGGAAACAATCTCTCTCACTCTGGCTCTAC 1471  
Qy 118 ThrlGlu-----LysArgPheThrPheMetArgPhe 126  
Db 1472 ACTAATAATGCTCTAGTAAACCCACACAAATAACGGCTAAAGAGTGTGGCTCA 1531  
Qy 127 ArgA-GlyLysAshIleSerTyrPheHisPheLeuVal----- 139  
Db 1532 AATGACCAAACTATGCTATACATCCAGAATTGCAAGAATTTCACATAACAAATGCT 1591  
Qy 140 -----PheAsnLeuLysValGlyAsnValThr-----ArgAspAlaAspAlaThrAsp 155  
Db 1592 ATGGAGGGCTAACCTATCACAAAGGTTAANGATAGGCAAGTGTGGCTCACTAA 1651  
Qy 156 IleGluAsnLeuLysValGlyAsnValThr----- 173  
Db 1652 ATGAAGGATTTCAGTACATCTCATACCATTTAACATCAGCTTGTATAAGAGCAT 1711  
Qy 174 Tyr-----ThrAsn 176  
Db 1712 CAGGATGAACTATTAGAAATTCCAAAATGAAATCTTGTGGATTAGCTGGTCAAGAAC 1771  
Qy 177 ValAspGluPheGly-----AlaSerPhePheAsnLysLeu 188  
Db 1772 ATCACAGACATGGAGCATTAATCACAGTGCACAGAATGCTCAACCAAAGTCAGT 1831  
Qy 189 SerPheThrThrGly----- 193  
Db 1832 CTATGACGCTGGGAGGGTCAATAAACGCACTCGTAGATAAAGGCCATATACTTC 1891  
Qy 194 -----LeuPheGlyTyrGlyIleLysArgAla 202  
Db 1892 CGTGAATCGAAATTGACCCCTGCTCAAGATTCCTGGTGTAAAGGCCATATACTTC 1951  
Qy 203 LeuLysGlnIleLeuLysArgAsnLeuProLeuAspIleGlyThrGluHsSerValSer 222  
Db 1952 CTA-----ATTGCTACTATATGCCGCAAGAGTACTCTCGAGAACCCGCACT 2002  
Qy 223 ArgLeuGlnIleThrSerSerTyrLysAspTyrMetAspThrGlnIleProLysLeu 242  
Db 2003 ACATTAAGGAT-----GCTTGAAAGCTAAACATTAAGGACAA-----CCGCAACTG 2053  
Qy 243 ProLysPheAlaLysArgPheSerLeuMet-----Val 253  
Db 2054 GGTTCATTATAATGAGGAAATTGTTAAATAATACTATGAAATTAGCAAAAGATT 2113  
Qy 254 ValGlnArgIleLeuAlaThrValAlaLys-----TyrValAspThrProTyr 270  
Db 2114 AAATCGATTAATCTCTACAAAGTCCAAAGGAAATATATGACCAAGATCACTAC 2173  
Qy 271 LysLysTrpTyrMetLysLeuLysAsnPhenylmetValAsnArgValPheIleProThrLys 290  
Db 2174 AAAAATTGAGCAGTGTAGAAAGTTATAAA-----ATGAGTT----- 2215  
Qy 291 LysPhePheAsnLysGluileArgGluProSerLysAlaLeuLysGluIysValSerThr 310  
Db 2216 -----CAAGAACTTAAGAGAAATTGAAAGTTGACAGAACATTG 2263  
Qy 311 AspThrLysAspLeuPheGluAsnLysIleGlyGlyGlyThrValAspPhePheAsnLys 330  
Db 2264 CTAGTAAAGATAATTGAACTTCATCAAAATTGCAATCTCAAAATTGC 2314  
Qy 331 GluIleArgAspProSerLysAlaLeu-----LysGlu 341  
Db 2315 CAATGAACTATGAAACTTACCATGAGCATTRAGGSCACACTAGATAAACAGCAT 2374  
Qy 342 LysValSerAsnAspAlaLysAspIlePheGluAsnLysIleGlyGlyGlyThr----- 359  
Db 2375 AAACGAAATTGAAATATCCGAT-----TTAATAACAACTGAGCTGACTGAGGTA 2431  
Qy 360 -----ValAspPhe----- 362  
Db 2432 ATGCAAATGGCCCTACATGATTAACAAAAAGAGACTGACCTTAATCAAAAGTTGA 2491

Alignment Scores:  
 Pre. No.: 0.000464 Length: 4766  
 Score: 119.50 Matches: 58  
 Percent Similarity: 46.11% Conservative: 31  
 Best Local Similarity: 31.35% Mismatches: 65  
 Query Match: 5.07% Indels: 31  
 DB: Gaps: 14

RESULT 7  
 PCT-US93-07261-10  
 Sequence 10, Application PCT-US93-07261  
 GENERAL INFORMATION:  
 TITLE OF INVENTION: P FEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREOF  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: John H. C. Blasdale  
 STREET: One Giralda Farms  
 CITY: Madison  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07440-1000

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh 6.0.5  
 SOFTWARE: Microsoft Word 5.1a  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT-US93/07261  
 FILING DATE: 19930805  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/927,531  
 FILING DATE: 07 AUG-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Blasdale, John H. C.  
 REGISTRATION NUMBER: 31,895  
 REFERENCE/DOCKET NUMBER: DDX288K  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-822-7398  
 TELEFAX: 201-822-7039  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4766 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 ORIGINAL SOURCE:  
 ORGANISM: Plasmodium falciparum  
 STRAIN: Malayan Camp  
 IMMEDIATE SOURCE:  
 CLOUSE: P2b1;P12-1  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 3...4766

RESULT 8  
 US-08-484-105-13  
 Sequence 13, Application US/08484105  
 ; Patent No. 5589341  
 GENERAL INFORMATION:  
 APPLICANT: STILLMAN, Bruce  
 APPLICANT: BELL, Stephen P  
 APPLICANT: KOBAYASHI, Ryuji  
 APPLICANT: RINE, Jasper  
 APPLICANT: FOSS, Margit  
 APPLICANT: McNALLY, Francis J  
 APPLICANT: LAURENSEN, Patricia  
 APPLICANT: HERSKOWITZ, Ira  
 APPLICANT: LI, Joachim J  
 APPLICANT: GAVIN, Kimberly  
 APPLICANT: GAVIN, Kimberly  
 TITLE OF INVENTION: ORIGIN OF REPLICATION COMPLEX GENES  
 NUMBER OF SEQUENCES: 24  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California

RESULT 9  
 US-09-807-459-2 (1-458) x PCT-US93-07261-10 (1-4766)  
 Sequence 9, Application PCT-US93-07261  
 GENERAL INFORMATION:  
 TITLE OF INVENTION: P FEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREOF  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: John H. C. Blasdale  
 STREET: One Giralda Farms  
 CITY: Madison  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07440-1000

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: Apple Macintosh  
 OPERATING SYSTEM: Macintosh 6.0.5  
 SOFTWARE: Microsoft Word 5.1a  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT-US93/07261  
 FILING DATE: 19930805  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/927,531  
 FILING DATE: 07 AUG-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Blasdale, John H. C.  
 REGISTRATION NUMBER: 31,895  
 REFERENCE/DOCKET NUMBER: DDX288K  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-822-7398  
 TELEFAX: 201-822-7039  
 INFORMATION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4766 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 ORIGINAL SOURCE:  
 ORGANISM: Plasmodium falciparum  
 STRAIN: Malayan Camp  
 IMMEDIATE SOURCE:  
 CLOUSE: P2b1;P12-1  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 3...4766

RESULT 10  
 PCT-US93-07261-10  
 Sequence 10, Application PCT-US93-07261  
 GENERAL INFORMATION:  
 TITLE OF INVENTION: P FEMP3 MALARIA ANTIGEN, ANALOGS, ANTIBODIES AND USES THEREOF  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: FLEHR, HOBACH, TEST, ALBRITTON & HERBERT  
 STREET: 4 Embarcadero Center, Suite 3400  
 CITY: San Francisco  
 STATE: California

ZIP: 94111-4197  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA: US/08/484,105  
 FILING DATE: 08/08/2007  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Osman Ph.D., Richard Aron  
 REFERENCE NUMBER: 36-627  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (415) 494-8700  
 TELEFAX: (415) 494-8771  
 TELEX: 910 27299  
 MOLECULE TYPE: CDNA  
 INFORMATION FOR SEQ ID NO: 13:  
 SEQENCE CHARACTERISTICS:  
 LENGTH: 327 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 ALIGNMENT SCORES:  
 Length: 3278  
 No.: 0.00283  
 Score: 111.00  
 Pos: 1  
 Aligned sequence:  
 5' AspSerValGlyAspValThrIysThrLeuLeuAlaAsnSerGluSerValAspSerAla 24  
 1214 GAGCTATATCAGATAATGAACTGGATTATCTGAATATCACGAAAGTAAGAGATT 1273  
 25 AlaAsnAlaTyrMetIleAsnSerAsp --- MetSerAspTyrLeuSerAlaValSer 42  
 1274 GAAACCGATCCCTCTGGACAGTGAAGAGTTGAAAGATTCAGCTGGAGAAG 1333  
 43 AspAsnPheAlaGluArgIleCysSerGlnVal----- 53  
 1334 CTGCAATGTGAGACCTGCCAAGAAAGGAGATCTATTAACAGATATACCCATT 1393  
 54 ---ProlySlySerAsnCysSerAlaSerValSerAlaTyrMetSer-----Arg 69  
 1394 TCCACGTTAAATCACAGACTCCATTGCCAGCCATCAGCACTTCATCTCTAGAAAG 1453  
 70 CysAlaLysGlnAspCysLeuIleLeuGlnSerLeuIlySlyTyrProLeuGluAlaLyst 89  
 1454 TCTTTAAGAAATATAGTGGCGCTAAAAGGCATATACTCCATTCTCCAAACGGTAT 1513  
 90 GluProLeuThrIleUroAspProTyroGlnLeuGluAlaAlaPheIleLeuPheLysGlu 109  
 1514 ArgAAATCCGAAGAATTCCTGACTGAACTGAACT 1558  
 110 SerAspAlaAsnProAlaAsnSerThrGluLysArgPheTrpMetArgPheArgGly 129  
 1559 AATAATGATTGCTGATAGCTGCAATTAGAGGAGATTCAGAACAGTTCAGCTAAAGGC 1618  
 130 LysAsnHisSerTyrPheHisAspLeuValPheAsnLeuLeuGluLysAsnValThrArg 149  
 1619 AAAATGGAGACATTTCCTAAGGTGAGAGCAATGAACTGCAAGGAAATGCAAAAGAA 1678  
 150 Asp---AlaAspAlaThrAspIleGluAsnPro---AlaSerArgTyrLeuTyMetAla 167  
 1679 GAAATGTCACAGCTGCTGATTCAGACATTCTCCGGCAAGAGAAATGAAATTGCA 1738  
 168 ThrLeuTyrTyrLysThrAspValAspGluIpheGlyAlaSerPhePheAsnLys 187  
 1739 AGTATTAACCTCTACTTACAGTGGATT---GAGCAGCCACTGACCCAGTATTAC 1795  
 188 LeuSerPheThrThrGlyLeuPheGlyTrpGlyLysArgAlaLeuLysGlnIleIle 207  
 1892 CAATACATGAAATCAATGGTTAACATTGTCACAGCAGACAAAAGACTTCAGATTC 1891  
 1952 TGGCAAAAATATCTGGAGAAAAGCTTACATCTGGAGCTGCCATGGATCTCTGGAGTT 2011  
 208 ArgSerAsnLeuProLeuAspIleGlyThr-----GluHissSerValSerAlaLeu 224  
 1847 AAG-----GATTAATGACATCTGCAAGCAGACAAAAGACTTCAGATTC 237  
 233 -----aspytMetAspThr 237  
 225 GlnHsIle----- 232  
 1892 GlnIle----- 257  
 2012 TATTTPACAAAGTTCGCTACGAAAAAGCTCTATCGTGTGTTATTGATGACTT 2071  
 258 LeuAlaThrValAlaGlyTyrValAspThrProTrp---TyrLysLysTrp-----Tyr 274  
 2072 GATGATATAGTTAGCAGAGCCAAAGATGTAATGTACACTCTTAATGGCTTACCTT 2131  
 275 MetLysLeuIysAsnHemMetVal-----AspArgValPheIleProThrLys 291  
 2132 TCAAATCGGAACATTATGTTGCTAGCCTGCACAAACCCATTAGCTCCCCAACGCCAT 2191  
 292 PhePheAsnLys----- 295  
 2192 CTTGGTGTACAAAGATTGGTCCAGAATGGTTTACTAGAATATGTCACTGGTACACG 2251  
 296 -----GluIleArg----- 298  
 2252 CATGAAAGCTAGAACATCATCATTTGAGACTTAATAATTGAAAGAATCTAGTTC 2311  
 299 -----GluProSerIysAlaLeuLysGluIysValSerThAspPheLysAspLe 316  
 2312 TATGTCACCCGGAGACAGGGAGTCTCACGATCTCCGGATACTAGTACTATA 2368  
 317 GluAsnLysIleGlyGlnGlyIleGlyThrValAspPhePheAsnLysGluIleArgAspProSer 336  
 2369 GAAACTGTGAGAGAAAAGGAAAGACTCTCAG-----TAT 2410  
 337 LysAlaLeuLysGluIysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGly 356  
 2411 AAACGACTAAACTTAGATTAATCTCTGATGCTGATGATGTCATGAAAGAAAATTGCT 2470  
 357 GlnGlyIleAspPheIleAsnAspGluIleArgAspProSerIysAlaLeuIleArg 376  
 2471 AGT-----GTCAGTGGGATGPGGGAGCTTAAAGGTTGTCAAAGA 2515  
 377 LysValSerThrGlyAlaGluAspLeu-----PheGluAsnLysIle--- 390  
 2516 GGGTAGAATATGCGGAATGATTACTAAAGAGGTTAGATGTCGACTAGTCAT 2575  
 391 -----GlyGlnGlyIleAspPheIleAsnAsnGluIleArg 402  
 2576 TCCAAAGAAGATCTAGTGGCAATGGTACAGGAATGAGAATTACAGGTTAGAATT 2635  
 403 ArgAspProSerLysAlaLeu 409  
 2636 AACATATTACAAAGGCTTA 2656



Qy 377 LysValSerThrGlyAlaGluAspIle-----PheGluAsnLysIle--- 390  
 ||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2516 GCGGTTAGAATGCGGAAATGATGTTACTAAAGAGCTTAGATATGAGCGACTAGTCAT 2575  
 Qy 391 -----GlyGlyLysValAspPheIleAsnAsnGluile 402  
 ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2576 TCCAAAAAGATACTAGTGGCAATGGTACAGGAATGAGATACAGAGTGAGT 2635  
 Qy 403 ArgAspProSerLysAlaLeu 409  
 ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|  
 Db 2636 AAGCAATTACCGAACCTTA 2656  
 RESULT 10  
 US-08-694-869-2  
 Sequence 2, Application US/08694869  
 ; Patent No. 594123  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olszewski, N.  
 ; APPLICANT: Tzairi, I.  
 ; APPLICANT: Somers, D. A.  
 ; APPLICANT: Lockhart, B.  
 ; APPLICANT: Torbert, K.  
 ; TITLE OF INVENTION: SUGARCANE BACILLIFORM VIRUS  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Schewe man, Lundberg, Woessner & Kluth, P. A.  
 ; STREET: P.O. Box 2938  
 ; CITY: Minneapolis  
 ; STATE: MN  
 ; COUNTRY: USA  
 ; ZIP: 55402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/694,869  
 ; FILING DATE: 09-AUG-1996  
 ; CLASSIFICATION: 800  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Woessner, Warren D  
 ; REFERENCE/DOCKET NUMBER: 30.440  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 612-373-6900  
 ; TELEFAX: 612-339-3061  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 7568 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: Genomic DNA  
 US-08-694-869-2  
 Alignment Scores:  
 Pred. No.: 0.0232  
 Score: 108.50  
 Percent Similarity: 34.95%  
 Best Local Similarity: 20.42%  
 Query Match: 4 60%  
 DB: 2  
 US-09-807-459-2 (1-458) x US-08-694-869-2 (1-7568)  
 Qy 51 SerGlnValProLysGlySerAsnCysSerAlaSerValSerAlaTyrMetSerArgCys 70

Db 1646 TCGAGAATCCAGGTCAAGGACTCTTCT-----AGGGTACCTCAGACGCC 1699  
 Qy 71 AlaLysGlnAsp-----CysLeuThrLeuGln-SerLeuLys 82  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1700 GAGGAGGAGACCTGGAGCTCTCATGCCACCTGATGTGGAGCTTACCGAGGCTGA 1759  
 Qy 82 S-----TyrProLeuGluAlaLysTyrGlnPro----- 91  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1760 GAGAGAGCCAGACTTCCAGCAGAGTCTGTATGGCCAGAGTGTATTC 1819  
 Qy 92 -----LeuThreIleProAspProTyrGlnLe 100  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1820 TCACAAAGTCTTCAGGGAGCTCTAGCCAGATTCCTCTGATGATGACAATAGCT 1879  
 Qy 100 uGluIalaAlaPheIleLeuPhelysGluSerAspAlaAsnProAlaAsnSerThrGluLys 120  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1880 TGATATGACCTTATC----- 1903  
 Qy 120 SargPheTerPheTerArgPheArgGlyLysAsnHisSerTyrPheHisAsp----- 137  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1904 AACATTGAGCAATGGAGCAGCAGGACTCGG-----TATATCATCCGAAATAC 1957  
 Qy 138 ----- 140  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 1958 AGCTGTAGATACTACAGCCTCTGCATCCAGCTGGTCAGGAAAACCTGGTTTCATAGTT 2017  
 Qy 140 easnLeuLeuGluLysAsnValThrArgPheAlaAspAlaThrAspIleGlu- AsnPh 159  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2018 CGGTGACATCAGAGTACCCACCAAGACTGGAGCTTCAGCACACAGATAAGGAT----- 2077  
 Qy 159 eAlaSerArgTyrLeuTyrMetAlaThrLeuTyrTyrLysThrTyrThrAsnValAspG 179  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2078 AGGACCAACAAATGGCTATGTCTATGCTCAATAGCTTCATGACACAGATAAGGAT----- 2129  
 Qy 179 upheGlyAlaSerPheAspLysIleSerPheIlePheIle-----GlyLeuPheG 196  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2130 -----TCCTTCATGGAAATCCAGCTACTGTCTACAGGAGCTTATGAGG 2176  
 Qy 196 YTRP---GlyIleIleLysArgAlaLeuIleGlyGlnIleIleArgSerAsnLeuPheLeuAspI 215  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2177 TTGGCAAGGA----- 2207  
 Qy 215 eGlyLysGluHisSerValSerArgLeuGluHisIleThrSerSerTyrLysAspTyrMe 235  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2208 -----AGGTGATAACTGGCAGATGTCATAACACACCAAGTGTATTCAGAT----- 2258  
 Qy 235 tasPheGlnIlePralaIleProLysPheIleIleArgSerAsnLeuPheLeuAspI 255  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2259 -----AAGGTGAGGAGTGGCGCTTATCACAAACCAAGTATAAGCTATG 2311  
 Qy 255 nargLeuLeuAlaThrValIleGlyLysValAspIleAspIleProIlePheIleAspIle 275  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2312 AGCCACTAAAGAGTGTAGAGGCACTCAGAGGAGGAGGAGAC----- 2357  
 Qy 275 tLysLeuLysAsnPheMetValAsnArgValAlaPheIleProIleLysPheIleAsnLys 295  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2358 ----- 2377  
 ;-----ATTCCGCCCTCAAAGCTA-----GA 2377  
 Qy 295 sGluIleArgGluProSerLysAlaLeuIleGluIleValSerThrAspIleLysAspIle 315  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2378 GGTAGTCATGCACCTTAC-----AAGGTGAGACTCA----- 2411  
 Qy 315 upHeGluAsnLysIleGlyLysIleGlyLysValAspPheIleProIleLysPheIleAsnLys 335  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2412 ---GAAATTATGATGCGCACACCTCTAGATCACAATATGAGGTCGCCAGTC 2467  
 Qy 335 oserLysAlaLeuLysGluIleValSerAsnAspIle 354  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||  
 Db 2468 TTCAAAGCCAGTAGAGCACAACCTCAGATGAGGAGGATATGGCCCTCTTGAAGAGA 2527  
 Qy 354 sIleGlyGlnGlyLysValAspPheIleAsnAsnGluIleIleArgAspProSerLysAlaLe 374  
 ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Db 2528 AGAGGAAGGGATGACATCACTTCTCTCACCGA AT 2533

Qy 374 uilearglysvaIserthrgly-----AlaGluAspIeupheGluAsnlystl 390

Db 2564 CTTATCAAGTACTCTACCCAGCAAAGTAGTGGAGAGAATTTCCCAAGAGA 2623

Qy 390 eGlyGlyGlyThrValAspPheIeAsnsh -----GluIear 403

Db 2624 AGACCAGATATTCGATTTCTGAAAGAACTGAAGAGCCTACCCGCTGAAATTGA 2683

Qy 403 gAsproSerLysAlaLeuIearglyValThrGluAlaAspAspIeupheGluas 423

Db 2684 AGAGAGAGACCCAGCGCTTAAGA-----CTGACAACTCATGAAAC 2728

Qy 443 aLeuIleArglyValSerThrGluAlaAspAlaLeuIe 456

Db 2768 AGTGAAGCTAAGTAGCAGCACIAGCATCTGCTA 2808

RESULT 11.

US-09-349-546-2

; Sequence 2, Application US/09349546

; GENERAL INFORMATION:

; PATENT NO. 609369

; APPLICANT: Olszewski, N.

; APPLICANT: Tzafir, I.

; APPLICANT: Somers, D.A.

; APPLICANT: Lockhart, B.

; APPLICANT: Tober, K.

; TITLE OF INVENTION: Sugarcane bacilliform virus promoter

; FILE REFERENCE: 600\_369US2

; CURRENT APPLICATION NUMBER: US/09/349, 546

; EARLIER APPLICATION NUMBER: US 08/694, 869

; EARLIER FILING DATE: 1996-08-09

; EARLIER APPLICATION NUMBER: PCT/IB97/01338

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 7568

; TYPE: DNA

; ORGANISM: sugarcane bacilliform virus

; US-09-349-546-2

Alignment Scores:

Pred. No.: 0.0232 Length: 7568

Score: 108.50 Matches: 97

Percent Similarity: 34.95% Conservative: 69

Best Local Similarity: 20.42%

Query Match: 4.608

DB: 3 3 Gaps: 24

US-09-807-459-2 (1-458) x US-09-349-546-2 (1-7569)

Qy 51 SerGlnValProIysGlySerAsnCysSerAlaSerValAlaTyrPheSerArgCys 70

Db 1646 TCTAGAGAATTCGCAAGTCAGCACTTGCTTCT-----ACGGGTACTTCAGACCC 1699

Qy 71 AlAlysGlnIasp-----CysIeuthrIeugly-SerLeuIy 82

Db 1700 GAGAGAGAGACCTGGAGATGCTCATGAGCCTGATGGAGGCTAACCCAGGAGCTAA 1759

Qy 82 s-----Tyr-ProleuGluAlaLysTyrGlnPro----- 91

Db 1760 GAGAGAGGCCAGAGCTTCAGCAGAGTCCTGAGAATGCTGAGATGATGATATCA 1819

Qy 92 -----LeutIleuProAspProTyroGlnle 100

Db 1820 TCACAAAGCTTCAGGGAGCTAGCCAGGATATCCCTCTGATGATGACAACTCAGCT 1879

Qy 100 uGluAlaAlaPheIeupheLysGluSerAspAlaAsnProAlaAsnSerThrGly 120

Db 1880 TGATATGACCTTATC----- 1880

Qy 120 sAlpGhePheArgPheArgArgGlyLysAsnHissertyPheHsAsp----- 137

Db 1904 AACATTGAGCANTGGAGCAGGAGACTCCGG-----TATATCATCCGGAAACT 1957

Qy 138 -----LeuValPh 140

Db 2018 CCGTGACATCAGAGATAACCCACCCAGAGTACTTGGAGCTATGGAAATGTGAGCA 2077

Qy 159 eAlaSerArgTyLeuTyMetAlaThrLeuTyTyRyStyTyRyRyAsnValAspI 179

Db 2078 AGGACCAAAATGGCTATGATCAATAGCTCTATGACAACGGTAAGGAT----- 2129

Qy 140 eAsnLeuIeuglyuAsnValThrArrAspAlaAspAlaThrAspIeupheGlu-----AspH 159

Db 2130 -----TCTTTCATGGAACTCCAGCTTACTGTCAGGTAAGGGTPTGAGG 2176

Qy 196 YTP-----GlyIeIeLysArgAlaLeuLysGlnIleIleargSerAsnLeuProIeupheAspI 215

Db 2177 TGGCAAGGA----- 2177

Qy 215 eGlyThrGluIhsSerValSerArgLeuIhnHsIlehrSerSerThrLysAspTyMe 235

Db 2208 -----AGGTGATAACTGCAAGATGTCAAATACAACCAATGTGATTTCAAGTAT 2258

Qy 235 tAspThrGlnIleProAlaLeuProIysPheAlaLysArgPheSerLeuMetValValG 255

Db 2259 -----AAGGTGAGGAGTGGCTCTTATCAGACCAAGGTATAAACGTTATG 2357

Qy 255 nArgLeuLeuAlaThrValAlaIleItyrValAspThrProTrtyrLysPheTrp 275

Db 2312 AGCCACTAAAGCTGGTGAAGGGCATAGAGGGAGATGGAC----- 2311

Qy 275 tLysLeuIysAsnRheMetValAsnArgValPheIeProThrLysPheAsnly 295

Db 2358 -----ATTCCTCCATCAAAGCTA-----GA 2377

Qy 295 sGluIleArgGluProSerLysAlaLeuLysGluIysValSerThrAspThrLysAspIe 315

Db 2378 GGTAGTCATGCAACCTACC-----AAGGTGAGCAGTACA----- 2411

Qy 315 uPheGluIuNlysIleGlyGlyGlyThrValAspPheAsnIysGluIleargGlyAspPr 335

Db 2412 -----GAAATTATGATGGCACAAACATCCAGTTCAAGTACAAATTATGAGGTGGCAGTC 2467

Qy 335 oSryLysAlaLeuIysGluIysValSerAsnAspAla--LysAspIeupheGluAsnly 354

Db 2468 TTCAAAAGCCAGTAGAGCACAACTCAGATGATGAGCATATGGCGCTTGTGAGA 2527

Qy 354 sIleGlyGlyGlyThrValAspPheIeAspIeupheGluAsnly 374

Db 2528 AGGAGAGGAGTCACATCACTTCTCACCGA----- 2528

Qy 374 uIlearglysvaIserthrgly-----AlaGluAspIeupheGluAsnlystl 390

Db 2564 CTTATCAAGTACTCTAGCAGCAAAGTAGTGGAGAGAATTTCCCAAGAGA 2623

Qy 390 eGlyGlyGlyThrValAspPheIeAsnsh -----GluIear 403

Db 2624 AGACCAATATTCGATTTCTGAAAAGACTGAGAAGCTACCCCTGCTGAAATTGA 2683

Qy 403 gAsproSerLysAlaLeuIleArglyValThrGluAlaAspAspIeupheGluas 423

Db 2684 AGGAGAGTACCCAGCGCTTAAGA-----CTGACAACTCATGAAAC 2728





Best Local Similarity: 21.18% Mismatches: 173  
 Query Match: 4.43% Index: 105  
 DB: 4 Gaps: 21

US-09-807-459-2 (1-458) x US-09-091-117-3 (1-4071)

QY 78 LeuGlnSerIleuLysTyrProLeuGluAlaLysTyrGlnPro-----Leu 92  
 Db 1023 TTAGGCCAAGAACGCGCTTAAGGATAACTCCAAGGGTAGTTGATAATTCTAAAGTAT 1082

QY 112 AlaAsn-----ProLalaAsnSerThrGluLysArgPheTrpMetAlaPheArgArgGly 129  
 Db 1083 GCGGANGGCCCTCCAGCGCTAACCCGCTAACGGTGTACGGAATGGTGTACCCACAGCTGTT 1142

QY 130 LysAsnHissTerPheHisAspIeLeuValPheAsnLeuLeuGluLysAsnValThrArg 149  
 Db 1143 AACCCAAACCAAGTTCTTGTATTA-----AGGCGCCAGCTCAACACTTACCCCT 1196

QY 150 AspAlaAspAlaThrAspIeGluAsnPheAlaSerArgTyrLeuTyrMetAlaThrLeu 169  
 Db 1197 TCATCGACACAAAGCTAGTTAGCTTACTTTATCTTCGCG----- 1225

QY 170 TyrTyrLysThrTyrIleAsnValAspGluPheGlyAlaSerPhePheAlaLysLeuSer 189  
 Db 1236 -----TTTACTAAC----- 1244

QY 190 PheThrThrGlyLeuPheGlyIleGluLysArgAlaLeuLysGlnIleLeuArg 209  
 Db 1245 TTACACGAACTCGTCTAGTGTAAACTACCCAGAGGTGATCGGTTGAGTGCCTC 1304

QY 210 AsnLeuProLeuAspIeGlyThrGluHisSerValSerArgLeuGlnHisIleThrSer 229  
 Db 1305 AACCAAGCTGTGTTACTATGTCATGCCATGGCTAGTGCACAAATATTAGTCTACCGCTG 1364

QY 230 SerTyrLysAsp-----TyrMetAspThrGlnIleProAlaLeuPro 243  
 Db 1365 TCTTACACAGATTACACTTGGTTAACTATATGTTGACCACTTTAACGGT 1424

QY 244 LysPheAlaLysArgPheSerLeuLeuThrValValGlnArgLeuLeuAlaThrValAlaGly 263  
 Db 1425 AAGGTGTGCTAAATATTAGTTAACCCCTCAAAACGATTAAACCTCGCC----- 1478

QY 264 TyrValAspThrProTrpTyrLysLysTrpTyrMetLysLeuLysAsnPheMetValAsn 283  
 Db 1479 -----TTAGCAAGCTTACATGGCTGTGTTGATGCAACCA 1520

QY 284 ArgValPheIleProThrLysPhePheAsnLysGluIleArgGluProSerLysAla 303  
 Db 1521 AAGAAATTAGTAGGTAAATCTCAACACCCACGCTGAG-----GCTGAGAC 1574

QY 304 LeuLysGluIleValSerThrAspThrLysAspLeuPheGlu----- 317

QY 328 AlaLeuLys-----GluIleValSerAsnASPAlaLysAspLeuPheGluAspLysIle 355  
 Db 1575 GTAAGGAGGACGTATGTCACATTGCAACATAAACCAATGACATGCCAAATATCGCT 1634

QY 338 AlaLeuLys-----GluIleValSerAsnASPAlaLysAspLeuPheGluAspLysIle 355  
 Db 1695 TTCCCTAAAGGTTAATGGATAAGTAAAGAATTTGAA----- 1751

QY 356 GlyGlyGlyIleValSerAspPheIleAsnLysGluIleArgAspProSerLys 337  
 Db 1635 GAGCTTAATGGCTAACGCCCTAAAGAATTTGCGATCACAAGAGGTCAACCTTAC 1694

QY 377 LysValSerThrGlyAlaGluAspIe-----PheGluAsnLysIleGly 392  
 Db 1525 AGTGCGAAATGGAACCTTGTACATCCAAATATTCCGAGAATCAAGTAAACAGG 1584

QY 393 GlyIleValAspPheIleAsnAsnGlu 401  
 Db 1585 GGAAAAATTGATGGAGTGAATTGGAA 1611

RESULT 14

US-09-091-117-3

QY 360 ValAspPhe-----IleAsnAsnGluIleArgAspProSerLysAlaLeuLeuArg 376  
 Db 1486 TTGGAATTCTATCACAAAGTGTAACTGAA-----TGCTGGAA 1524

GENERAL INFORMATION:

APPLICANT: The University of Melbourne

TITLE OF INVENTION: Mycoplasma Recombinant Polypeptides and

NUMBER OF INVENTIONS: Vaccines

CORRESPONDENCE ADDRESS:

ADRESSEE: GREENLEE, WINNER and SULLIVAN P.C.

STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder

STATE: Colorado

COUNTRY: United States of America

ZIP: 80303

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/091,117

FILED DATE: 12 JUNE 1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/AU96/00803

FILED DATE: 13-DEC-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: AU PNT127

FILED DATE: 13-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: WINNER, ELLEN P.

TELECOMMUNICATION INFORMATION:

TELEPHONE: +1 303 499 8080

TELEFAX: +1 303 499 8089

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 4071 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: Linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Mycoplasma pneumoniae

FEATURE:

NAME/KEY: CDS

LOCATION: 250..654

FEATURE:

NAME/KEY: CDS

LOCATION: 762..3851

OTHER INFORMATION: /codon=(seq: "tga" 3648..3651, aa: Trp)

OTHER INFORMATION: /codon=(seq: "tga" 3663..3665, aa: Trp)

OTHER INFORMATION: /codon=(seq: "tga" 3663..3665, aa: Trp)

US-09-091-117-3

Alignment Scores:

Pred. No.: 0.026 Length: 4071

Score: 104.50 Matches: 93

Percent Similarity: 36.67% Conservative: 68



SEQUENCE CHARACTERISTICS:  
 LENGTH: 2134 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE: NAME/KEY: CDS  
 LOCATION: 127..1956  
 ; US-08-799-138-3

Alignment Scores:  
 Pred. No.: 0.021 length: 2134  
 Score: 101.50 Matches: 68  
 Percent Similarity: 34.70% Conservative: 67  
 Best Local Similarity: 17.48% Mismatches: 127  
 Query Match: 4.30% Indels: 127  
 DB: 2 Gaps: 17

US-09-807-459-2 (1-458) x US-08-799-138-3 (1-2134)

QY 139 ValPheAsnLeuGlulSasnValThrArgAspAlaThrAspIleGluAsn 158  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 844 GTTGTGCAATGATCATCACACAGACATAACAGAAGCTGCTAGCT 903  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 159 PheAlaSerArgTyrLeuTyRMetAlaThrLeuTyRLeuTyRLeuAsn 178  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 904 AGAGAACGTTGACTAC---TCAATAGTACCCGTGAAATATAACCTGG 954  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 179 GluPheGlyIAlaSerPhePheAsnLysLeuSerPheThrArgIleGly 198  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 955 AGATGGGTTCGGAGCATCTGGCGAAGATG 984  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 199 IleLysArgAlaLeuIysGlnIleLeuArgSerAsnLeuProLeuAspIleGlyThrGlu 218  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 985 CTCTCAAGAACGATTTGCAAGCACTAATCAGAAGCTTCAATTCCT 1035  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 219 HisSerValSerArg 223  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1036 TCTCTTAATTAAACAAACAAATGCTGAACTGAACTGTTAGAAAGCT 1095  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 224 -----LeuGlnIleThrSerSer----- 230  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1096 GTACGAGCTGATGCCIGGGGAAGTGTATGCAATCATGGAATATGCCCTCATTTGAT 1155  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 231 -----TyrLysAspTyrMet----- 235  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1156 CAATATTAAGAACGATCTTGATGCCGCTGGGCCCTGGAGGTTGATAAATTTATAATGTC 1215  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 236 ---AspThrGlnIleProAlaLeuProLys-----PheAlaLysArgPheSerLeu 251  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1216 TTGACAAATCAGCTCCCGCTGCTTAATAAAGGTGTCAGTTGATAGCAGCTTCATG 1275  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 252 MetValValGlnIargIleLeuAlaThrValAlaGlyTyr-----ValAspThrPro 268  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1276 GAAATATAGAACTTACTGAACTGATGGCTATGCCCTCATCTTATAGCTCA 1335  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 269 TrpTyrLysLysTrpTyrTymetIysLeu-----LysAsnPhmetValAsnArgValPheIle 287  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1336 ---GACANGGATATCCGTCGCTPATGTCATCTCTTAAATCT----- 1377  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 288 ProThrLysPhePheAsnLysGluIleArgGluProSerLysAlaLeuIysGluLys 307  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1378 -----ATTAGGGCCCTGCTGAGGCAGCTGTTGAGCG 1410  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 308 ValSerThrPhePheAspLeuPheGluAsnLysIleGlyGlnGlyLysValAspPhe 327  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1411 GTCACGTGCTGCTTAAGGACTTGGTTCAC----- 1440  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 328 PheAsnLysGluIleArgAspProSerLysAlaLeuIysGluLysValSerAsnAspPhe 347  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1441 -----AAAGCTTACGTGAGACTTGGCTGAGCG 1473  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  

RESULT 17  
 US-09-392-362-3  
 Sequence 3, Application US/09392362  
 ; Patent No. 6248868  
 GENERAL INFORMATION:  
 APPLICANT: Verma, Dush, Pal  
 TITLE OF INVENTION: PHRAGMOPLASTIN  
 NUMBER OF SEQUENCES: 6  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CALFEE, HALTER & GRISWOLD  
 STREET: 800 SUPERIOR AVENUE  
 CITY: CLEVELAND  
 STATE: OHIO  
 COUNTRY: USA  
 ZIP: 44114  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PATENTIN Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/392,362  
 FILING DATE:  
 CLASSIFICATION:  
 PRIORITY APPLICATION DATA:  
 APPLICATION NUMBER: US/08/799,138  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GOIRICK, MARY E  
 REGISTRATION NUMBER: 34,829  
 REFERENCE/DOCKET NUMBER: 227/27/00139  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (216) 622-8458  
 TELEFAX: (216) 241-0816  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2134 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE: NAME/KEY: CDS  
 LOCATION: 127..1956  
 ; US-08-799-138-3

QY 348 LysAspIlePheGluAsnLysIleGlyGlnGlyLysValAspPheIleAsnAsnGluIle 367  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1474 TATCCGGTCRCCGGGTGAGCTGGGCTCTGCCTGTTGATTCATA---GAAGAAATG 1530  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 368 ArgAspProSerLysIleAlaLeuIleArgLysValSerThrGlyAlaIleAspIlePheGlu 387  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1531 AGGATGAAAGCAA-----AGGAAACACTGCACTAGTTGAT 1569  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 388 AsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluIleArgLysProSerLys 407  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1570 ATGGAGCTGGCTATCTGACTGTGTTGATTCCTCTGGAAAGCTCTCAAGATGTTGATAG 1629  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 408 Ala-----LeuIleArgLysValTrpThrGluAlaAspAspIlePheGluAsnLysIle 425  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1630 GGTGGCAATCCCACATTCAATTGATAGATATAATGATTCTATCTAGGGCAATT 1689  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 426 GlyGlyIleGlyThrValAspPheIleAsnLys----- 435  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1690 GGACCCACAATTGTCATAGTCATAATGGCTGCTGCTGACTGGGAATTCATTC 1749  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 436 -----GluIleArgAspProSerLysIleAlaLeuIleArgLysValSer 449  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1750 AAGTCCATCGTCATTTGTCAGATGATTCATATCTAGGGCAATT 1809  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 QY 450 ThrgIleAlaAspAsnIleLeuGluIle 458  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 1810 ACCGACCTAGGCAAATGGAGACCAAG 1836



OY 159 eAlaserArgTyrLeuTyrmetaLathrLeuTyrmlysthrTyrmlysthrThrAsnValAspG1 179  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 Db 479 GGGTICATCICAAACATATATT---TTGTTAGGCTATCCACAAAGCACAGAG--- 530  
 ; Sequence 1, Application US/08565907A  
 ;  
 Oy 179 uPheGlyAlaSerPhePheAsnLysLeuSerPheThrThGlyLeuPheGlyTrpGlyI 199  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 Db 531 .....-.....-ATAGTCATGCAAATATAGCTGGAGCTTT-----AT 562  
 ;  
 Oy 199 eLysArgAlaLeuLysGlnLeileArgSerAsnLeuProLeuAspIleGlyThrGluH1 219  
 ||| ||| ||| ||| ||| ||| ||| ||| |||  
 Db 563 ATTAAGACTTGAAATCATGAGATACATT 598  
 ;  
 Oy 219 sservalserArgLeuLnhisIerhrserSerTyrmlyAspTyrmMetAspThrGlnI1 239  
 ||| ||| ||| ||| ||| ||| ||| |||  
 Db 599 TGCTTAATACGATTATCATTATACAGGC-----AA 629  
 ;  
 Oy 239 eProAlaLeuProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuAl 259  
 ;  
 Db 630 .....-.....-GTTATTTCTAACATTAC 649  
 ;  
 Oy 259 AthrValAlaGlyTyrmValAspThrProTyrmlyLysTrpTyrmMetAspThrGlnI1 279  
 ||| ||| ||| |||  
 Db 650 AACGCTCTTGGCTT----- 665  
 ;  
 Oy 279 nPhenetylValAsnArgValPheIleProThrLysPhePheAsnLysGluIargG1 299  
 ||| ||| ||| ||| ||| |||  
 Db 666 -TCTTATCGTCAGAAATACAAACCTTAAAGCTTAAAGCTTAAAGACGCTAACGGTGT 724  
 ;  
 Oy 299 uProProLysAlaLeuLysGluLysValSerThrPheAspPhe-----GA 772  
 ||| ||| ||| ||| ||| |||  
 Db 725 ATCTGAGGGATTACTCTTAAACCTTCTGTCACAAACGAAAT 319  
 ;  
 Oy 319 sIleGlyGlyLysThrValAspPhe-----PheAsnLysGluIleArgAspProSerly 337  
 ||| ||| ||| ||| |||  
 Db 773 ATTGCTCAATATGGCCGATATCAGATGAGTCAGAAGCTGAGTCAGAAGCGAAGCTGA 832  
 ;  
 Oy 337 salAlaLeuLysGluLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleGlyI 357  
 ||| ||| ||| ||| ||| |||  
 Db 833 CGCATTA-----TCCACACTAAATAATATAGAGACGCTTAATTACTCTATGCTGTA 886  
 ;  
 Oy 357 nGlyThrVal----- 361  
 ||| |||  
 Db 887 AGGTGCTCTAGGTTAAATGAGAGTCGACAATATCTATCTAAATAAGATGGCGATGA 946  
 ;  
 Oy 361 pPhelLeAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValSerThrG1 381  
 ||| ||| ||| ||| |||  
 Db 947 TATTGAGCAATATGATGAGCTAAAGCTTCTTAATGAAATT----- 998  
 ;  
 Oy 381 yAlaGluAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnG1 401  
 ||| ||| ||| ||| ||| |||  
 Db 999 ---GAAGAACTTTAACTAAAA-----CAACGGA 1027  
 ;  
 Oy 401 uIleArgQAsP-----ProSerLysAlaLeuIleArgLysValSerThrG1 412  
 ||| ||| |||  
 Db 1028 ATGGCTGATTTAGAAATGATGACGAGCTTGTGAGACCAAGCTATTCATAA 1087  
 ;  
 Oy 412 s-----ValTyrmGluAlaAspAspLeuPheGluAs 423  
 ||| |||  
 Db 1088 GATTGACACAGGGAGGTTAAAGTGGTGCTGAGTCAGTGAGATGACTATGAGCA 1147  
 ;  
 Oy 423 nLysIleGlyGlnGlyThrValAspPhe-----AsnLysGluIleArgAspPhe 440  
 ||| ||| ||| |||  
 Db 1148 CAATCTAGATCAATGAAAGAAAGTTCTGATGATCACATGAATTAACGACACC 1207  
 ;  
 Oy 440 o-----SerLysAlaLeuIleArgLysValSerThrGluAlaAs 453  
 |||  
 Db 1208 TATATCATTACTACAAAGTTATCAGATCATGATGTTACAGAAACGGA 1267  
 ;  
 Oy 453 pAsnIleLeuGlu 457  
 ;  
 Db 1268 TGAATTAAGAA 1280  
 ;

RESULT 19  
 US-08-565-907A-1  
 ; Sequence 1, Application US/08565907A  
 ;  
 ;  
 GENERAL INFORMATION:  
 APPLICANT: Sylvain Moineau, Barbara  
 APPLICANT: J. Holler, Peter A. Vandenberghe,  
 APPLICANT: Ebenezer R. Wedamuthu, Jeffrey K.  
 APPLICANT: Kondo  
 APPLICANT: Kondo  
 TITLE OF INVENTION: DNA Encoding Phage  
 TITLE OF INVENTION: Abortive Infection Protein  
 TITLE OF INVENTION: From Lactococcus  
 TITLE OF INVENTION: From Lactococcus  
 NUMBER OF SEQUENCES: 1  
 NUMBER OF SEQUENCES: 1  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Ian C. McLeod  
 STREET: 2190 Commons Parkway  
 CITY: Okemos  
 STATE: Michigan  
 COUNTRY: USA  
 ZIP: 48864  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette 5.25 inch,  
 COMPUTER: Acer  
 MEDIUM TYPE: 360 Kb storage  
 OPERATING SYSTEM: MS-DOS (version 4)  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/565, 907A  
 APPLICATION NUMBER: US/08/565, 907A  
 FILING DATE: December 1, 1995  
 CLASSIFICATION: 435  
 PRIORITY APPLICATION NUMBER:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ian C. McLeod  
 REGISTRATION NUMBER: 20, 931  
 REFERENCE/DOCKET NUMBER: Quest 4.1-152  
 SEQUENCE CHARACTERISTICS:  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (517) 347-4100  
 TELEFAX: (517) 347-4103  
 TELEX: No. 5814499e  
 INFORMATION FOR SEQ ID NO: 1:  
 DESCRIPTION: Genomic DNA  
 LENGTH: 4467  
 TYPE: Nucleotide  
 STRANDEDNESS: Single  
 TOPOLOGY: Linear  
 MOLECULE TYPE:  
 DESCRIPTION: Genomic DNA  
 HYPOTHETICAL: No  
 ANTI-SENSE: No  
 FRAGMENT TYPE: N/A  
 ORIGIN: Lactococcus lactis  
 ORGANISM: Lactococcus lactis  
 STRAIN:  
 INDIVIDUAL ISOLATE: w1  
 DEVELOPMENTAL STAGE: N/A  
 HAPLOTYPE: N/A  
 ORIGINAL SOURCE:  
 TISSUE TYPE: N/A  
 CELL TYPE: bacterium  
 CELL LINE: N/A  
 ORGANELLE: N/A  
 IMMEDIATE SOURCE:  
 LIBRARY: genomic  
 CLONE: SNO-20  
 POSITION IN GENOME: N/A  
 FEATURE:  
 NAME/KEY: phage abortive infection  
 LOCATION: N/A  
 IDENTIFICATION METHOD: sequencing  
 OTHER INFORMATION: DNA encoding phage  
 OTHER INFORMATION: resistance







Db 2274 GAATRAGGGAGCTAAATGTTTCCAGTTATAACAAATACATGAAACAAA- 2311  
 Qy 308 1SerthrAphrLysAspIe-..... 3115  
 Db 2332 -AAGTAGATACTAAATATAGCAATCTTTCGAAAAGAACATGGTTACCAATT 2310  
 Qy 315 -..... 3115  
 Db 2391 TAACTGTTGAAAAATATTAGTTATCATTAAAGATTCAAGATTCAGATTAGTT 2450  
 Qy 316 -.....PhGlu-.....AsnLysIleGlyGlnGlyThrValAspPheAsn- 329  
 Db 2451 TTGACTTCTTGAAATATTAGTTATCAGTTAGTTCAAGTTCAGTTACATAAGTT 2450  
 Qy 330 -.....LysGluIeArgAspPheAsn-..... 329  
 Db 2511 TGTRAAAATATTTAGTTATACTAACTAACTAATGTTAAATATGAGTT 2510  
 Qy 347 aLYSAspLeuPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnGluI 367  
 Db 2571 TAAGATAATTTATCAGAAATATCAATGTTGTTGTTGCTCTGAAAT 2630  
 Qy 367 eARASp-.....proSerLysAlaLeuLeuArglyValSerThrGlyAlaGluAspIe 385  
 Db 2631 AGAGATTATAATCAAGAGAACTAACTAATGTTAAATATGAGTT 2690  
 Qy 385 uPheGluAsnLysIleGlyGlnGlyThrValAspPheIleAsnAsnGluI 405  
 Db 2691 T-.....TCTTAATTTAGGCTACGATTTCATCAGAT-..... 2727  
 Qy 405 oSerLysAlaLeuIeArglyValTyRThrGluAlaAspIeLeuPheGluI 423  
 Db 2728 -AGTICATATAATTGAAAAATTTAAAGATCAATTATTAT 2781  
 RESULT 22  
 US-08-229-781-27  
 ; Sequence 27, Application US/08229781  
 ; PATENT NO. 5589174  
 ; GENERAL INFORMATION:  
 ; APPLICANT: YOSHINOBU OKUNO et al.  
 ; TITLE OF INVENTION: ANTI-HUMAN INFLUENZA VIRUS ANTIBODY  
 ; NUMBER OF SEQUENCES: 58  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Wenderoth, Lind & Ponack  
 ; STREET: 805 Fifteenth Street, N.W., #700  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: Wordperfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/229,781  
 ; FILING DATE: April 19, 1994  
 ; CLASSIFICATION: 530  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: 08-054 016  
 ; FILING DATE: April 29, 1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warren M. Cheek, Jr.  
 ; REGISTRATION NUMBER: 33,367  
 ; REFERENCE/DOCKET NUMBER:  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-371-8850  
 ; TELEFAX:  
 ; INFORMATION FOR SEQ ID NO: 27 :  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1754 base pairs

Alignment Scores:  
 Pred. No.: 0.0269 Length: 1754  
 Score: 99.50 Matches: 59  
 Percent Similarity: 35.328 Conservative: 37  
 Best Local Similarity: 21.568 Mismatches: 89  
 Query Match: 4.22% Indels: 85  
 DB: 1 Gaps: 13

US-09-807-459-2 (1-458) x US-08-229-781-27 (1-1754)

Qy 195 PheGlyPheGlyIleLysArgAlaLeuLysGlnIleLeuArgSerAsnLeuProLeuAsp 214  
 Db 852 TTGGTCAGGA-.....-ATCATCCTCAACGCCATCAGTT 890  
 Qy 215 IleGlyThrGluHisSerValSerArgLeuGlnHisIleThrSer-.....TyrIys 232  
 Db 891 GAATGTTGACCGGAAGGTCAACACCCACGGGCTATAACAGTGTCTTCCTTCAG 950  
 Qy 233 AspTyrMetAspThrGlnIleProAlaLeuProLysPheAlaLysArgPheSerLeuMet 252  
 Db 951 ATGTCACCCAGTCACAATAGGAGCTGTCAAAGTGTCTCAGGAGTACAATAAATAG 1010  
 Qy 253 ValVal-.....-GlnArgLeuLeuAlaThrVal 261  
 Db 1011 ATGGTTACAGGACTAGGACATCCATCATTCACTCAGAGGTGTTGGACCAAT 1070  
 Qy 262 AlagItyTyraLysPheProTrp-.....-TyrLysLysTrpTrp-..... 274  
 Db 1071 GCGGGTTCACTGAAAGGGGGTGGACTGGATGATAGATGATGATGTTATGCTATCAT 1130



QY 393 GlyThrValAspPheIleLeasnAsnGlu 401  
 ::::||| :::: |||  
 Db 1563 GAAAAATTGATGGAGTGAATGGAA 1589

RESULT 24  
 US-09-004-422-27  
 ; Sequence 27, Application US/09004422  
 ; Patent No. 6337070  
 ; GENERAL INFORMATION:  
 ;  
 ; APPLICANT: Yoshinobu OKUNO et al.  
 ; TITLE OF INVENTION: POLYPEPTIDES FOR USE IN GENERATING  
 ; NUMBER OF SEQUENCES: 58  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSE: Wenderoth, Lind & Ponack, L.L.P.  
 ; STREET: 2033 K Street, N.W., #800  
 ; CITY: Washington, D.C.  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20006  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: MS DOS  
 ; SOFTWARE: WordPerfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/004,422  
 ; FILING DATE: January 8, 1998  
 ; CLASSIFICATION: 530  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/443, 862  
 ; FILING DATE: May 22, 1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/229, 781  
 ; FILING DATE: April 19, 1994  
 ; REFERENCE/DOCKET NUMBER:  
 ; APPLICATION NUMBER: 08/054, 016  
 ; FILING DATE: April 29, 1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warren M. Cheek, Jr.  
 ; REGISTRATION NUMBER: 33, 367  
 ;  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1754 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA to genomic RNA  
 ; HYPOTHETICAL:  
 ; ANTI-SENSE:  
 ; FRAGMENT TYPE:  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: *A/Su1ta/1/89*  
 ; STRAIN:  
 ; INDIVIDUAL ISOLATE:  
 ; DEVELOPMENTAL STAGE:  
 ; HAPLOTYPE:  
 ; TISSUE TYPE:  
 ; CELL TYPE:  
 ; CELL LINE:  
 ; ORGANELLE:  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY:  
 ; CLONE:  
 ; POSITION IN GENOME:  
 ; CHROMOSOME/SEGMENT:  
 ; MAP POSITION:

QY Alignment Scores:  
 Pred. No.: 0.0269 Length: 1754  
 Score: 99.50 Matches: 58  
 Percent Similarity: 35.32% Conservative: 37  
 Best Local Similarity: 21.56% Mismatches: 89  
 Query Match: 4.22% Indels: 85  
 DB: 4 Gaps: 13

US-09-807-459-2 (1-1458) x US-09-004-422-27 (1-1754)

QY 195 PheGlyTrpGlyIleLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAsp 214  
 ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::|||  
 Db 852 TTGGGGTCAGAA-----ATCATCCTCAAACGATCATATGG 890  
 QY 215 IleGlyThrGluHisSerValSerArgLeuGlnHisIleThrSer----TyrLys 232  
 ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::|||  
 Db 891 GATGTGACCGAAGGTGTCACAAACCCCCAGGGAGCTAAACAGCAGTCCTTCAG 950  
 QY 233 AspTyrMetAspThrGlnIleIleProLeuProLysPheAlaLysArgPheSerLeuMet 252  
 ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::|||  
 Db 951 ATGTGACACCCAGTCACAAAGAGGTGTCACAAAGTATGTCAGGAGTCAAATTAAGG 1010  
 QY 253 ValVal-----GlnArgLeuLeuIleThrVal 261  
 ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::|||  
 Db 1011 ATGGTTTACAGACTAAAGAACATCCCATCCATTCAATCCAGGTTGGTGGAGCCATT 1070  
 QY 262 AlaGlyTyrValAspThrProTrp-----TyrLysLysTrpTyr----- 274  
 ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::|||  
 Db 1071 GCGGGTTCTATGAGGGGGTGGACTGGATGATGATGATGATGATGTTATCATCA 1130  
 QY 275 -----MetLysLeuLysAsn 279  
 ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::|||  
 Db 1131 CAGAATGAAACRAGGATCTGCTATGCTGGCATCAAAACACACACACACAAATGCCATTAC 1190  
 QY 280 PheMetValAsnArgVal-----PheIleProThr 289  
 ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::|||  
 Db 1191 GGAATTACAAACAAAGGTGAACTCTGTAATGAGAAATGAGACACTAACATTCACAGCTG 1250  
 QY 290 LysLysPhePheAsnLysGluIleArgGlnProSerLysAlaLeuLysGluLysValSer 309  
 ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::|||  
 Db 1251 GCGAAAGAAATTCACAAA-----TTACAAAGAGGAGTGAATCTTAATAAAAGTTGAT 1307  
 QY 310 ThrasPheLysAsp-----LeuPheGluAsnLys 319  
 ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::|||  
 Db 1308 GATGGATTCTGGACATTTGACATATAATCCAGAATGTTGCTACTGGAAAT--- 1364  
 QY 320 IleGlyGlnGlyIleValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeu 339  
 ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::|||  
 Db 1365 -----GAAGAGGACTTGTGTTCTGATGTCATAATGTTGAGAAATCTGTGTTGAGAAAGA 1418  
 QY 340 LysGluLysValSerAsnAspAlaLysAspIlePheGluAsnLysIleGlyGlnGlyIle 359  
 ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::||| ::::|||  
 Db 1419 AAAGCCAAATTAAAGATAATGCCAAAGAA-----ATAGATACGGGT 1463

QY 360 ValAspHe-----IleAsnAsnGluIleArgAspProSerLysAlaLeuIleArg 376  
Db 1464 TTTGAACTCTACCAACAGTGTACATGAA-----TGCAGGAA 1502  
QY 377 LysValSerThrGlyAlaGluAspLeu-----PheGluAsnLysIleGlyGln 392  
Db 1503 AGTGTTGAAAATGGAACTTATGACTTCCAAATATTCCGAGGAACTCAAAGTAAACAGG 1562  
QY 393 GlyThrValAspHelleAsnAsnGlu 401  
Db 1563 GAAAATGATGGAGGAAATGGAA 1589

RESULT 25  
US-09-308-375-1  
; Sequence 1, Application US/09308375  
; Patent No. 630017  
; GENERAL INFORMATION:  
; APPLICANT: Genencor International, Inc.  
; TITLE OF INVENTION: Proteases From Gram-Positive Organisms  
; FILE REFERENCE: GC194-PC1  
; CURRENT APPLICATION NUMBER: US/09/308, 375  
; EARLIER APPLICATION NUMBER: EP9719636, 4  
; EARLIER FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FASTSEQ for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 7100  
; TYPE: DNA  
; ORGANISM: *Bacillus subtilis*  
; US-09-308-375-1

Alignment Scores:  
Pred. No.: 0.315  
Score: 99.00  
Percent Similarity: 43.61%  
Best Local Similarity: 21.64%  
Query Match: 4.20%  
DB: 4

US-09-807-459-2 (1-458) x US-09-308-375-1 (1-7100)

QY 188 LeuSerPheThrThrGlyLeuPheGlyTrpGlyLysArgAlaLeuLysGlnIleIle 207  
Db 5585 GTGAGCTACAGAACAACTTGTCTAACTAAAGTTGATGAGACACTAAAGTCATCAGTCA---TTG 5641  
QY 208 ArgSerAsnLeuProLeuAspIleGlyThrGluHissValSerArgLeuGlnHissIle 227  
Db 5642 AAAGTCATCTCTTAAACCCAAAGGAAATTAAGATGTCGATAACAAATTCAATG 5700  
QY 228 ThrSerSerTyrIleASP-----TyrMetAspThrGlnIleProAlaLeu----- 242  
Db 5701 ACAGCAAGAGATGAGACAGGTTAACTATAGCAAGCAATAAACGTCATTCAACAA 5760  
QY 243 ---ProLysPheAlaLysArgPheSerLeuMetValValGlnArgLeuLeuIlaThrVal 261  
Db 5761 CRACCAAAGGAACCGAACAAATCAATTAAAGCAGCTTGAGAACAAAGAACCT---GCG 5817  
QY 262 AlaGlyTyrIleAsp-----ThrProIlePheLysIleProAlaLeu----- 276  
Db 5818 AAAGGTTTCCCTGACATCCAGGACAGATCAGGAAATGCAACACTGGAAAGATCAA 587  
QY 277 LeuIysAsnPheMetValAsnArgValPheIleProThrLysIlePheAsnLysGlu 296  
Db 5878 CAGAAAGTTT-----AACCTTGAGCTTATACACCAAG-----AAAGTCG 5919  
QY 297 IleArgGluProSerLysAlaLeuLysGluLysValSerThrAspThrLysAspLeuIle 316  
Db 5920 ATCAAGGATATCTATATACATGCTGATGAGTTGATCCATCTACAAAGGAGATGTC 5979  
QY 317 Glu-----AsnLysIleGlyGlyGlyIleGlyThrValAsp 326

RESULT 26  
US-08-743-637B-169  
; Sequence 169, Application US/08743637B  
; Patent No. 5994066  
; GENERAL INFORMATION:  
; APPLICANT: BERRERON, Michel G.  
; APPLICANT: PICARD, Francois J.  
; APPLICANT: OUELLETTE, Marc  
; APPLICANT: ROY, Paul H.  
; TITLE OF INVENTION: SPECIES-SPECIFIC AND UNIVERSAL DNA  
; TITLE OF INVENTION: PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND  
; TITLE OF INVENTION: IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED  
; TITLE OF INVENTION: ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS ...  
; NUMBER OF SEQUENCES: 273  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OQUARLES & BRADY  
; STREET: 411 EAST WISCONSIN AVENUE  
; CITY: MILWAUKEE  
; STATE: WISCONSIN  
; COUNTY: USA  
; ZIP: 53202-4497  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/743, 637B  
; FILING DATE: 04-NOV-1996  
; CLASSIFICATION: 435  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: US 08/526, 840  
; FILING DATE: 11-SEP-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BAKER, Jean C.  
; REGISTRATION NUMBER: 35,433  
; REFERENCE/DOCKET NUMBER: 850586, 90012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (414) 277-5000

Db 5980 GAAAAATGCGGATATGAGTTAGAACGGCATCGAAAAGGACTCAGACTTGATCGAT 6039  
QY 327 PhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGlu---LysValSerAsn 345  
Db 6040 GAGATAGCAAG---ACTGATGACGAGGCTAAATTCAAAAGAATTAAAGAAACCAA 6096  
QY 346 AspAlaLysAspBleuPheGluAsnLysIleGlyGlnLysValAsp-----Phe 362  
Db 6097 GACAGTATTCACAAAGTGACIGACGACCAATTACATCTCTGATGATCTGAACTC 6156  
QY 363 IleAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValSerThrGlyAla 382  
Db 6157 GGAAGAGTCAAAGTCAAGAGCTAACIGACAGCTT---CAAAGAGCAGTTAGACCT 6213  
QY 383 GluAspIlePheGluAsnLysIleGlyGlnGlyThrValAppHelleIleAsnAsnGlu 402  
Db 6214 GATGATTTCTAAAGGATTCGCAAAGTACACAAACGGAAAGAGGCGCTCAAGATCAGCTC 6273  
QY 403 ArgAspProSerLysAlaLeuIleArgLysValTyrrHgluAlaLysPasp----- 419  
Db 6274 GAAAAGATGAGGAGTCATCACATATATACATGATATCTGTTAATGAGAACGAGCC 6333  
QY 420 -----LeuPheIleAsnLysIleGlyGlnGlyThrValAspHelleIleAsnLysGluIle 437  
Db 6334 TTTAAAAGCTGAGGATAAGATTAATGATGATGAAAGAACGATATGCTAACGACTT 6393  
QY 438 ArgAspProSerLysAlaLeuIleArgLysVal-----SerThrGluIleAsp 453  
Db 6394 AAATGATTTCTGAGTTATATACCAATATGGAGTCATTTGAAAGATTTCAAC 6453



QY 203 LeuLysGlnLeuLeuArgSerAsnLeuProLeuAspIleGlyThrGluHisSerValSer 222  
 :::::::::::::::::::::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 706 --AATGAAACAGAAAGTGTAACTATCCTCTAGAAAGGCACTCACATCATTAGT 762  
 :::::::::::::::::::::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Qy 223 ArgLeuGlnHisIleThrSer-----SerrTylysAspTyrmEtaP 236  
 :::::::::::::::::::::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 763 TATCTGGCTCCCTTACTCTGAAGAATTAAACAAAGAAATAAAGCTTAAGAT 822  
 :::::::::::::::::::::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Qy 237 -thrglnileProAlaIuProlysPheAlaLysArgPheSerLeuMetValValGlnAr 256  
 :::::::::::::::::::::|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 823 GATCCAGTAA-----TNGGTAANAGGACTCG----- 850  
 :::::::::::::::::::::|||:|||:|||:|||:|||:|||:|||:  
 Qy 256 gleLeuIaLathValAlaGlyTyrvAlaSpIrrProTyptTylysLysTrpTyrMetly 276  
 :::::::::::::::::::::|||:|||:|||:|||:|||:|||:|||:|||:  
 Db 850 ----- 850  
 :::::::::::::::::::::|||:  
 Qy 276 sLeuLysAsnPhenMetValAsnArgValPheIleProThrLysPhePheAsnLysG1 296  
 :::::::::::::::::::::|||:|||:|||:|||:|||:|||:|||:  
 Db 851 ---AAANACTT-----ACGATAAAAGCTCCACATGAA 882  
 :::::::::::::::::::::|||:  
 Qy 296 uIleArgGluProSerLysAlaLeuLysGluLysValSerThrAspThrLysAspLeuH 316  
 :::::::::::::::::::::|||:|||:|||:|||:|||:|||:|||:  
 Db 883 GATGCTATCAGTCACATCTGTCGAC-GATAATAGCAATACATGCAACATACATTAAT 941  
 :::::::::::::::::::::|||:|||:|||:|||:|||:  
 Qy 316 eGluAsnLysIleGlyGngLysThrValAspPhePheAsnLysGluIleArgAspProSe 336  
 :::::::::::::::::::::|||:|||:|||:|||:|||:  
 Db 942 AGAGAAANAG-----AAAANGATGCCAANGATATCA 974  
 :::::::::::::::::::::|||:  
 Qy 336 rLysAlaLeuLysGluLysValSerAsnAspAlaLysAspLeuPheGluAsnLysIleG1 356  
 :::::::::::::::::::::|||:|||:|||:  
 Db 975 ACTAACTATGATGCTAAAGTCAAAAGAGTATTAAACAACTGAAATGATTATGG 1034  
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 Qy 356 ygIgngLysThrValAspPheIleAsnAsnGluIleArgAspProSerLysAlaLeuIle 376  
 :::::::::::::::::::::|||:|||:|||:  
 Db 1035 CTCAGGATCTGCT-----ATCCACCTTCACACAGGTGAATTATAGC 1076  
 :::::::::::::::::::::|||:  
 Qy 376 gLysValSerThrGlyAlaLysGluIleAspLeuPheGluAsnLysIleGlyGngLysThr 396  
 :::::::::::::::::::::|||:  
 Db 1077 ACTGTAGACACCTCTCATATGACGTCATCCATTATGTTGCAAGAACGAA 1136  
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 Qy 396 pPheLeuAsnAsnGluIleArgAspProSerLysAlaLeuIleArgLysValTyrrThri 416  
 :::::::::::::::::::::|||:  
 Db 1137 ATAT--ATAAATTAACCGAAGTAAAAAGACCTGCTAACAGTCCAGATAC 1193  
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 Qy 416 uAlaAspAspPheLeuPheGluAsnLysIleGlyGngLysThrValAspPheIleAsnLysG1 436  
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 Db 1194 AACCTCACCGGTTCACTCAAAATAATTAAACGCAATGATGGTTAAATACAAAC 1253  
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 Qy 436 uIleArgAsp 439  
 :::::::::::::::::::::|||:  
 Db 1254 ATTAGACGAT 1263  
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 RESULT 28  
 US-08-688-988-9  
 Sequence 9, Application US/08688988B  
 ; PATENT NO. 609645  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lefebvre, Daniel D.  
 ; APPLICANT: Malboobi, Mohammad A.  
 ; TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS  
 ; FILE REFERENCE: PPL96-03  
 ; CURRENT APPLICATION NUMBER: US/08/688,988B  
 ; CURRENT FILING DATE: 1996-07-31  
 ; NUMBER OF SEQ ID NOS: 48  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 1829  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; US-08-688-988-9  
 ;  
 Alignment Scores:  
 Pred. No.: 0.0511 Length: 1829

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Db 1303 GGATATGGAGAACTAGGGCCCTCAGARTCTGTCGCTGTCGACATATAAC 1362
QY 362 -----PheIleAsnAsnGluIleIleArgAspProSerLysAlaLeu--IleArgLys 377
Db 1363 AGAAATATTCATCTCAGAGGCATCTTTCAGTATGTCAGAGGAGCTTGCATCCAAA 1422
QY 378 ValSer---ThrGlyAla-----GluAspLeu 385
Db 1423 GTGAATGTTACAGGATACTTGTATGGTCACTTGAGTGGCAAGATGGT 1482
QY 386 PheGluAsnIleIleGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 405
Db 1483 TACAAACAGATTGCTACTGACTAGTGTGATTCAAATACTCACAGT 1536
QY 406 SerLysAlaLeuIleIleArgLysValThrGluAlaAspAspLeuPheGluAsnIle 425
Db 1537 -----TACGAGAAGATCC 1551
PCT-US93-03077-2
; Sequence 2, Application PC/rUS9303077
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; APPLICANT: Gaynor, Richard B.
; APPLICANT: Wu, Foon Kin
; TITLE OF INVENTION: PROTEIN CELLULAR FACTOR USEFUL FOR
; TITLE OF INVENTION: REGULATING GENE EXPRESSION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patient Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PC/rUS93/03077
; FILING DATE: 19900331
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/862,025
; FILING DATE: April 2, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kammerer, Patricia A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: UFFD270PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-787-1540
; TELEFAX: 713-749-2679
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3279 base Pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; PCT-US93-03077-2
Alignment Scores:
Pred. No.: 0.134
Score: 97.50
Percent Similarity: 33.67%
Length: 3279
Matches: 99
Conservative: 66

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Best Local Similarity: 20.20%
Query Match: 4,138
Mismatches: 196
Indels: 130
Gaps: 19
DB: US-09-807-459-2 (1-458) x PCT-US93-03077-2 (1-3279)
QY 9 AspValThrLysThrLeuLeuAlaAlaSerGluSerVal-----AspSerAlaAla 25
Db 1135 GAAGTAAATGAAACATAGTATACCCACGAGGAGCAATGGAGAAAGTGACGA 1194
QY 26 AsnAlaTyroIleIleSerAspMetSerAspTyroLeu--SerAlaValSerAspAsn 44
Db 1195 ATGCACTCTGTTACTGTGACACGCCATATCTGTTCTGTTCTACACCAATAAT 1254
QY 45 PheAlaGluArgLysSerGlySerGlySerAsnCysSerAlaSerValSer 64
Db 1255 GAAGGACAGACTGTGTTAGAGAAGGT-----GCAGGAGGTGAACTGTGAGA 1308
QY 65 AlaTyMetSerArgCysAlaLysGlnAsp--CysLeuThrLeuGlnSerLeuLysTyr 83
Db 1309 CAGCCAGAAAGCAGTTCGTGAGGAAGGAGCTTGCAAGCAGTGTGAA 1368
QY 84 ProLeuGluAlaLys---TyrGlnProLeuThrLeu---ProAspProTyroGlnLeuGlu 101
Db 1369 AACCTGCAAAAAGGGAGGCTCAGTTATCTCTAGTAGAGGAAAGGACTCTGAGA 1428
QY 102 AlaAlaPheIleLeuPheLysGlu-----SerAspAlaAsnProAla 115
Db 1429 GAAGCTTGTATAACCTGAAAGATGAAATGTCAGAGTGAAGAAGAAGAAGCAGTGTGATT 1488
QY 116 AsnSerThrGluLysArgPheTyrMetArgPheAlaArgGlyLysAsnHisSerTyrPhe 135
Db 1489 TCTTCCTGAAAGATGAGTGTACTCAAGAATGAGCA----- 1530
QY 136 HisAspLeuValPheAsnLeuLeuGluLysAsnVal-----ThrArgAsp 150
Db 1531 -----GAAAGAAAGTCACAATAGCCCTGCAGAGAGAGAT 1566
QY 151 AlaAspAlaThrAspIleGluAsnPheAlaSerArgTyrLeuTyMetAlaThrLeuTyr 170
Db 1567 GCTGCTAAAGAGAACATAAACATAAAAGAAAGAA----- 1602
QY 171 TyrLysThrTyrrhkrksnValAspGluPheGlyAlaSerPhePheAsnLysLeuSerPhe 190
Db 1603 CTGTCACACTGATTAATAGTAGTGAACACTGCAAGCTTGTGAAGAAGAAGATGAGCAG 1662
QY 191 ThrThrGlyIlePheGlyTyrGlyLysArgAlaLeuLeuGlnThrIleLeuArgSerAsn 210
Db 1663 ATCCGAGGGTTATGGAGAAAGGAAACCTTCACAAACAGCAGGTGCAACATCTAC 1722
QY 211 Leu-----ProLeuAspIleGlyThrGluHisSerValSerArgLeuGln 225
Db 1723 ATCATCAAGAAATTAAGAGCTAAAGACAAAGGAGAAATATGGTTGCAAGCAG 1782
QY 226 HisIleThrSerSerTyroLysAspTyrMetAspThrGlnIleProAlaLeuProLysPhe 245
Db 1783 AAAAAGTTAAGAGCTGAGGAGGTG----- 1812
QY 246 AlaLysArgPheSerLeuMetValValGlnArgLeuLeuAlaThrValAlaGlyTyrVal 265
Db 1813 -----CAGCATGAAACGGTCTTGATGCC----- 1839
QY 286 PheIleProThrLysAspPheAsnLysGluIleArgGluProSerLysAlaLeuLys 305
Db 1840 -----AAAGAGGTGAGAACACATAGGAAATAATAAAACTAAT 1887
QY 266 AspThrProTrpTyrLysLysTrpTyrMetLysLeuLysAsnPheMetValAsnArgVal 285
Db 1839 ----- 1839
QY 306 GluLysValSerThrAspThrLysLysAspLeu----- 315
Db 1888 TCCATGGTAGAACGCCAAGGAAAGATCTGGCCGCTTCAGGTAGACATGGATGACTT 1947

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Query Match:		4.11%	Indels:	100
		4	Gaps:	16
RESULT 34				
QY	139	ValPheAsnLeuLeuGluLysAsnValThrArgAspAlaSpaLpheThrAspIleGluAsn	158	US-09-807-459-2 (1-458) x US-09-392-362-5 (1-2211)
Db	892	GTGTTGAAATAGATCACACAGACATAACAGAAAGATGTTGACATGATGTTGCTGCTAGGCGT	951	08-094-889-2
Qy	159	PheAlaSerArgTyrLeuTy-MetalathioneTyLeuTyLysThrTyThrAsnValAsp	178	Sequence 2, Application US/08094889
Db	952	AGAGAACGTTGATGCT--TWAATGACTACCTGTAAATAAACCTGGAAAC-----	1002	Patent No. 5470966
QY	179	GlupheGlyAlaSerphepheAsnLysLeuSerphepheThrThrGlyLeupheGlyTrpGly	198	GENERAL INFORMATION:
Db	1003	AGAATGGTCTGACATCCTGGCGGANGATG-----	1032	APPLICANT: Shinji HIRANO et al.
QY	199	IleLysArgAlaLeuLysGlnIleIleArgSerAsnLeuProLeuAspIleGlyThrGlu	218	TITLE OF INVENTION: NEURAL 'C-ATENIN
Db	1033	CTCTCAAAGATTTGGAGACAGTAACTCAAGTCAAATTCCT-----GGCATTCAA	1083	NUMBER OF SEQUENCES: 2
QY	219	HisSerValSerArg-----	223	CORRESPONDENCE ADDRESS:
Db	1144	GTGAGCTGATGCTGGGAAAGTGATGCTATCATGGAAATATGCCCTCATGTG	1203	ADDRESSEE: Wenderoth, Lind & Ponack
QY	231	-----TyrLysAspTyrMet-----	235	STREET: 805 Fifteenth Street, N.W., #7000
Db	1204	CAATAATTAAAGACCATCTTGATGGCGTGCGGCTGGAGGTGATAAAATTATATGTC	1263	CITY: Washington
QY	236	--AspThrGlnIleProAlaLeuProLys-----	251	STATE: D.C.
Db	1264	TTCGACAACTAACGCTCCTGCTTGCTTAAGAAAGGTGCAAGTGTGATGAGCCTTCATG	1323	ZIP: 20005
QY	252	MetValValGlnIargLeuAlaLpheValAlaGlyTyr-----	268	COMPUTER READABLE FORM:
Db	1324	GAAATATAGGAAACTTATGACAAAGCAGTGGATGAGCTCATCTAAATGCTCCA	1383	MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
QY	269	TrpTrpLysLysTrpTyrMetLysLeuLysAsnpheMetValAsnArgValPheIlePro	288	COMPUTER: IBM Compatible
Db	1384	-----GAACRAGGATACCTGCGCTTATGAACTTCTTATAACTATAGGGCCCT	1437	OPERATING SYSTEM: MS-DOS
QY	289	ThrLysLysPhepheAsnLysGluIleArgGluProSerLysAlaLeuLysGluLysVal	308	CURRENT APPLICATION DATA:
Db	1438	GCTGACTCACTGTGTATG-----GCGGTCAGTCCTGTTAAAGACTTGTTGTCACAGCT	1494	APPLICATION NUMBER: US/08/004, 889
QY	309	SerThrAspIleArgLysAspLeu-----	323	APPLICATION NUMBER: US/08/004, 889
Db	1495	ATGAGTGAGACTTGGACTTGCAAGCAGTATCTGGCTCCGGGTGAGGTGGGCTGCA	1554	TELEFAX: 202-371-8850
QY	324	ThrValAspPhePheAsnLysGluIleArgAspProSerLysAlaLeuLysGluLysVal	343	TELEPHONE: 202-371-8850
Db	1555	TCTGTTGATCCTGAAAC-----ATGAGGGATGAAGCMA-----	1593	TELEFAX: 202-371-8850
Qy	344	SerAsnAspAlaLysAspLeuPheGluLysLysIleGlyIleGlyIleGlyThrValAspPheIle	363	SEQUENCE CHARACTERISTICS:
Db	1594	--AGGCAACACTGAGCTAGTGATGATGAGTGCTACTGACTGTGATTCTT	1650	SEQUENCE: 3123 base pairs
Qy	364	AsnAsnGluIleArgAspProSerLysAla-----LeuIleArgLysValSerThrGly	381	TYPE: nucleic acid
Db	1651	CGGAAGCTTCTCAAGATGTTGATAAAGGGTGGCAATGCCACATCAATTGTGATAGA	1710	STRANDEDNESS: double
Qy	382	AlaGluAspIlePheGluLysLysIleGlyIleGlyIleGlyThrValAspPheIleAsnIle	400	SEQUENCE LENGTH: 3123 base pairs
Qy	401	-----	405	TOPOLOGY: linear
Db	1711	TATAATGATTCATCTAAGCGCAATTGGGACCAATTGTCATGTCATGTCATGTC	1770	MOLECULE TYPE: cDNA to mRNA
QY	401	-----	405	HYPOTHETICAL: ANTI-SENSE:
Db	1771	TGTGCTACTTGCGGCAATTCCAACTCCATGTCATGTCATGTCATGTC	1830	FRAGMENT TYPE: ORIGINAL SOURCE:
QY	401	-----	405	ORGANISM:
Db	1771	TATAATGATTCATCTAAGCGCAATTGGGACCAATTGTCATGTCATGTCATGTC	1770	STRAIN:
QY	401	-----	405	INDIVIDUAL ISOLATE:
Db	1771	TGTGCTACTTGCGGCAATTCCAACTCCATGTCATGTCATGTCATGTC	1830	DEVELOPMENTAL STAGE:
QY	401	-----	405	HAPLOTYPE:
Db	1771	TGTGCTACTTGCGGCAATTCCAACTCCATGTCATGTCATGTCATGTC	1830	TISSUE TYPE:
QY	401	-----	405	CELL TYPE:
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QY	401	-----	405	ORGANELLE:
Db	1771	TGTGCTACTTGCGGCAATTCCAACTCCATGTCATGTCATGTCATGTC	1830	IMMEDIATE SOURCE:
QY	401	-----	405	LIBRARY:
Db	1771	TGTGCTACTTGCGGCAATTCCAACTCCATGTCATGTCATGTCATGTC	1830	CLOSE:
QY	401	-----	405	POSITION IN GENOME:
Db	1771	TGTGCTACTTGCGGCAATTCCAACTCCATGTCATGTCATGTCATGTC	1830	CHROMOSOME/SEGMENT:
QY	401	-----	405	MAP POSITION:
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QY	401	-----	405	PUBLICATION INFORMATION:









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 QY PROTHIOLYSYPHEPHEAASNLYSGLIULEARGLUPROSERLYSALALEULYSGLIULYS 307  
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 Db 1087 CCTACA-----CCTCTAATACHTTCTCTAATCTTAATGCAAAGTTAAAGGA 1137  
 QY 308 VALSERTHRASPHTHRLYSGLIUPHEGLIUNSLYSILEGLYGLYGLYRVALASPHE 327  
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 Db 1138 AGTGATGAAAGATGCCAATGATGATTGCGAGCTAACAGGACATGATGATTGGTT 1197  
 FILING DATE: 23-MAR-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/218, 018  
 FILING DATE: 25-MAR-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/307, 057  
 FILING DATE: 25-MAR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Spruill, W. Murray  
 REGISTRATION NUMBER: 32,943  
 REFERENCE/DOCKET NUMBER: CGC 1695/CIP3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-541-8615  
 TELEFAX: 919-541-8619  
 INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2612 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 118..2484  
 OTHER INFORMATION: "note" "Native DNA sequence  
 US-08-463-483A-31  
 Sequence 31, Application US/08463483A  
 Patent No. 5849870  
 GENERAL INFORMATION:  
 APPLICANT: Warren, Gregory W  
 APPLICANT: Koziel, Michael G  
 APPLICANT: Mullins, Martha A  
 APPLICANT: Nye, Gordon J  
 APPLICANT: Carr, Brian  
 APPLICANT: Desai, Nalini M  
 APPLICANT: Kostichka, N. Kristy  
 APPLICANT: Duck, Nicholas B  
 APPLICANT: Estruch, Juan J  
 TITLE OF INVENTION: No. 5849870el Pesticidal Proteins and Strains  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESSEES:  
 ADDRESSEE: CIBA-GEIGY Corporation  
 STREET: 7 Skyline Drive  
 CITY: Hawthorne  
 STATE: NJ  
 COUNTRY: USA  
 ZIP: 10532  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30B  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/463,483A

RESULT 39  
 US-08-471-046A-31  
 Sequence 31, Application US/08471046A  
 patent No. 586326  
 GENERAL INFORMATION:  
 APPLICANT: Warren, Gregory W  
 APPLICANT: Koziel, Michael G  
 APPLICANT: Mullins, Martha A  
 APPLICANT: Nye, Gordon J  
 APPLICANT: Carr, Brian  
 APPLICANT: Desai, Nalini M  
 APPLICANT: Kostichka, N. Kristy  
 APPLICANT: Duck, Nicholas B  
 APPLICANT: Estruch, Juan J  
 TITLE OF INVENTION: Method For Isolating Vegetative  
 TITLE OF INVENTION: Protein Genes  
 NUMBER OF SEQUENCES: 50  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: No. 586326artis Corporation  
 STREET: 3054 Cornwallis Road  
 CITY: Research Triangle Park  
 STATE: NC  
 COUNTRY: USA  
 ZIP: 27709  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30B  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/471,046A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
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 APPLICATION NUMBER: US 08/463,483  
 FILING DATE: 05-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/314,594  
 FILING DATE: 09-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/218,018  
 FILING DATE: 23-MAR-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/037,057  
 FILING DATE: 25-MAR-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Meigs, J. Timothy  
 REGISTRATION NUMBER: 38,241  
 REFERENCE/DOCKET NUMBER: CGC1695/CIP3/DIV8 - SQLv4  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 919-541-8587  
 TELEFAX: 919-541-8689  
 INFORMATION FOR SEQ ID NO: 31:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2612 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 HYPOTHETICAL: NO  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 118..2484  
 OTHER INFORMATION: /note= "Native DNA sequence  
 OTHER INFORMATION: encoding VIP3a(b) from AB424"  
 US-08-471-046A-31  
 Alignment Scores: 0..123  
 Aligned: 95..50  
 Score: 95..50  
 Matches: 102  
 Percent Similarity: 36..188  
 Conservative: 80  
 Best Local Similarity: 20..288  
 Mismatches: 202  
 138 LeuIvalPhe---AsnLeuLeuGluLysAsnValThrArgSpaLeuAspAlaThrAspIle 156  
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||  
 673 TTAACCTTGTCTACAGAAACTAGTCAAAAGTAAAGATGGCTCTCCCTGCAGATAT 732  
 157 GluAsnPheLeaSerArgTrpLeuTrpMetAlaThrLeuTrpTrpLysTrpTrpThrAsn 176  
 ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||  
 733 CGTGTAGACTAACGAGTTACTGACTAGTACGAAAGACTTAACAAAATGATGAGAT 792  
 177 ValAspGluPheGlyAlaSerPhePheAspLeuSerPheThrThrGlyLeuPheGly 196  
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 793 GGTGTTGAAATTACCTTAATACATCCAGATGATGGTAGGAATAATTATTCGGG 852  
 ---TrpGlyIleLysArgAlaLeuLysGlnIleLeuArgSerAsnLeuProLeu---- 213  
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 853 CGTTCAAGCTTAAACTGCATCGGAATTATTACTAAAGAAATGCTGAAACAACTGGC 912  
 214 ---AspIleGlyIleGluHisSer-----ValSerArgLeuGluIleHisIleThr 228  
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 913 AGTGAAGTCGAAAGTTAACTCTTAACTGATTACAGCTCTGAA 963  
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 964 -----GCAAAAGCT 972  
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 1087 CCTTACAC-----CTTATCTAACTCTTCTAACTCTTATGCTAAAGTTAAAGGA 1137  
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 328 PheAsnLysGluIleArgAspProSerLysIleLeuLysGluValSerAsnAspIle 347  
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 348 -----LysAspLeuPheGluAsnLysIleGlyGlnGlyIleValAspPheIleAsn 364  
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 1216 ATTACAGTATTAAGATATATGAGCTTAACCTAAACAA-----AAT 1257  
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 1309 AATATTGTCGCCAGATCACTCTGGACAA-----ATCTTATACAAATAACATA 1359  
 403 ArgAspProSerLysAlaLeuIleArgLysVal----- 413  
 ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||  
 1360 GTATTTCAGAAATGAGATGATTAATGATCTAAATGATGATCTAACTAAAAATGAAACCTTA 1419  
 ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||  
 414 ---TyThrGluIalaAspAspPheGluAsnLysIleGlyGlnGlyIleValAspPhe 432  
 ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||  
 1420 AGATATGAGGTTAACAGCGGAAATTATGATCTCTTACAGAGAA-----ATTGAC--- 1470  
 ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||  
 433 IleAsnLysGluIleArgAspProSerLysIleLeuIleArgLysValSerThrGluAla 452  
 ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||  
 1471 TTAATTAAGAAAAGTAGATCAAGTGAAGCGGGAGTATGAAACCGTTAAGTGCTATATGAT 1530  
 453 AspAsnLeu 455  
 ||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::||| ::|||  
 1531 GATGGGTG 1539  
 PREV 118..2484  
 OTHER INFORMATION: /note= "Native DNA sequence  
 OTHER INFORMATION: encoding VIP3a(b) from AB424"  
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